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OM protein - protein search, using sw model

Run on: October 31, 1999, 07:01:30 ; Search time 13.26 Seconds
(without alignments)
894.928 Million cell updates/sec

Title: US-09-297-092-1
Perfect score: 2673
Sequence: 1 MRLPKLLTFLWYLAWLDE.....ANNVYKQYEDMVVSCGCR 501

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2673	100.0	501	1 R69600	New TGF-beta famil
2	2673	100.0	501	1 W12770	Human bone morphog
3	2673	100.0	501	1 W01799	Human MP52 protein
4	2673	100.0	501	1 W11900	Human high mol. wt
5	2673	100.0	501	1 W19210	Human TGF-beta pro
6	2673	100.0	501	1 W36100	Human MP52. Produc
7	2673	100.0	501	1 W33008	Human MP52. Mouse
8	2673	100.0	501	1 W44868	TGF-beta superfam
9	2630	98.4	501	1 R95635	Cartilage-derived
10	2400	89.8	495	1 R60022	Growth differentia
11	2133	79.8	401	1 R40800	TGF-beta-like clon
12	905.5	33.9	436	1 R95636	Cartilage-derived
13	771	28.8	321	1 R78730	Human mature VL-1
14	771	28.8	321	1 W26591	Human bone morphog
15	660	24.7	263	1 R78739	Murine mv2 protein
16	660	24.7	263	1 W26595	Murine BMP-13 homo
17	658	24.6	120	1 R78731	Murine protein MP5
18	658	24.6	388	1 R78734	Human bone morphog
19	658	24.6	120	1 W26590	Human MP52 protein
20	658	24.6	388	1 W26592	Human bone morphog
21	654	24.5	119	1 W06920	Human MP52 growth
22	654	24.5	119	1 W19846	Human bone inducin
23	606	22.7	294	1 R78729	Human bone morphog
24	606	22.7	294	1 W26589	Human bone morphog
25	595	22.3	411	1 R78740	Fusion of BMP-2 pr
26	595	22.3	411	1 W26597	BMP-2 propeptide/B
27	573	21.4	134	1 R66867	Gdf-6. Growth diff
28	544	20.4	240	1 R78738	Murine mv1 protein
29	544	20.4	240	1 W26594	Murine BMP-12 homo
30	510	19.1	161	1 W54057	Gdf-7 C-terminal r
31	503	18.8	129	1 R65108	Bone morphogenetic
32	449.5	16.8	396	1 R51653	Prepro human BMP2
33	443.5	16.6	396	1 R44747	Osteogenic protein
34	443.5	16.6	396	1 R85762	Human BMP2A. Anti
35	443.5	16.6	396	1 W44303	Human osteogenic p
36	443.5	16.6	396	1 W89680	Human osteogenic p
37	441.5	16.5	396	1 R47255	Pre-pro-BMP2. Worp
38	440.5	16.5	396	1 R80619	Human Bone Morphog
39	440.5	16.5	396	1 R14241	Human BMP-2A encod
40	440.5	16.5	396	1 R29281	Human pre-pro-BMP-
41	440.5	16.5	396	1 R36732	Human BMP-2. Recom
42	440.5	16.5	396	1 W15404	Human BMP-2A. Prot
43	440.5	16.5	396	1 W24849	Human bone morphog

STROUP
091297092
SEQ ID:1

p-selectin ligand
BMP2A/2B fusion pr

44 439 16.4 437 1 W53323
45 437.5 16.4 400 1 R15474

ALIGNMENTS

RESULT 1

R69600 standard; Protein; 501 AA.

AC R69600;
DT 10-OCT-1995 (first entry)
DE New TGF-beta family member - MP-52 protein sequence.
KW transforming growth factor-beta family; mitogenic; differentiation;
KW treatment; prevention; disease; bone; cartilage; connective tissue;
KW skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
KW tissue regeneration; arthritis; ss.
OS Homo sapiens.
FH key Location/Qualifiers
FT peptide 382
FT /label= mature protein

PN W09504819-A.

PD 16-FEB-1995.

PF 09-AUG-1994; E02630.

PR 10-AUG-1993; DE-326829.

PR 25-MAY-1994; DE-418222.

PR 09-JUN-1994; DE-420157.

PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.

PI Hotten G, Neidhardt H, Paulista M, Hoetten G;

DR WPI: 95-090897/12.

DR N-PSDB: Q83695.

PT New DNA encoding a new member of the TGF beta family - and
PT related vectors, host cells etc., has mitogenic and
PT differentiating inducing activity, e.g. for treating or
PT preventing diseases of bone and cartilage etc.

PS Claim 6; Page 36; 51pp; German.

CC The amino acid sequence of a novel member of the transforming growth
CC factor-beta (TGF-beta) family named MP-52. The gene encodes a protein
CC of 501 amino acids (AA). The protein, or at least the mature protein,
CC has mitogenic and/or differentiation inducing properties useful in
CC the treatment or prevention of diseases of bone, cartilage, connective
CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
CC be used for wound healing and tissue regeneration e.g. in osteoporosis
CC and arthritis.

CC Sequence 501 AA;

SQ

Query Match 100.0%; Score 2673; DB 1; Length 501;

Best Local Similarity 100.0%; Pred. No. 1.6e-191;

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 MRLPKLLTFLWYLAWLDEICTVLGAPDLGQRPGQTRGLAKAEKERPLARNVFRP 60

Db 1 MRLPKLLTFLWYLAWLDEICTVLGAPDLGQRPGQTRGLAKAEKERPLARNVFRP 60

QY 61 GGHSGGGATNANARAKGGTGTGGLTPQKDEPKLPPRPGGPEPKPPQTRQATAR 120

Db 61 GGHSGGGATNANARAKGGTGTGGLTPQKDEPKLPPRPGGPEPKPPQTRQATAR 120

QY 121 TVTPKGOLPGGKAPPKAGSVPSFLKKAREPGPPPEKPEKPPPTTPHEYMLSLVRTL 180

Db 121 TVTPKGOLPGGKAPPKAGSVPSFLKKAREPGPPPEKPEKPPPTTPHEYMLSLVRTL 180

QY 181 SDADRKGGNSVSKLEAGLANTITSFDKGGDDRGVPVVRKQRYVFDISALEKDGLLGAELR 240

Db 181 SDADRKGGNSVSKLEAGLANTITSFDKGGDDRGVPVVRKQRYVFDISALEKDGLLGAELR 240

QY 241 ILRKPSDTAKPAAPGGGAAQLKSSCPGSGROPASLLDVRSPGLDGSWEVFDIWKLF 300

Db 241 ILRKPSDTAKPAAPGGGAAQLKSSCPGSGROPASLLDVRSPGLDGSWEVFDIWKLF 300

QY 301 RNFKNASQLCLEAEWGRGAVDLRGLGFDRAAROVHEKALFLVFGRTKRDLPFNEIKA 360

Db 301 RNFKNASQLCLEAEWGRGAVDLRGLGFDRAAROVHEKALFLVFGRTKRDLPFNEIKA 360

Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360
 QY 361 RSGQDDKTVYELFSQRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420
 Db 361 RSGQDDKTVYELFSQRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420
 QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480
 Db 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480
 QY 481 SANNVYKQYEDMVVESCGR 501
 Db 481 SANNVYKQYEDMVVESCGR 501

RESULT 2
 ID W12770 standard; Protein; 501 AA.
 AC W12770:
 DT 11-MAY-1997 (first entry)
 DE Human bone morphogenic factor MP52 Arg.
 KW Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
 KW connective tissue; mucous membrane; epithelium; teeth;
 KW wound healing; vulnary; tissue regeneration; osteoporosis;
 KW bone fracture; dental implant; osteoblast.
 OS Homo sapiens.
 FH Key
 FT peptide
 FT 1. 27
 FT /label= Sig_peptide
 FT cleavage_site
 FT 380. 381
 FT /note= "sequencing suggests MP52 Arg is processed
 proteolytically at Arg380-Arg381"
 FT cleavage_site
 FT 381. 382
 FT /note= "alternative cleavage site at Arg381-Ala382"
 FT mat_protein
 FT 381. 501
 FT /label= Mat_protein
 FT /note= "mature MP52 Arg preferred for use in
 compns. of the invention"
 FT
 PN W09706254-Al.
 PD 20-FEB-1997.
 PF 02-AUG-1996; E03427.
 PR 03-AUG-1995; EP-112241.
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
 PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
 DR WPI: 97-154261/14.
 DR N-PSDB; T59729.
 PT New human bone morphogenic factor, MP52 Arg - used in the treatment
 of osteoporosis and bone fracture, and for promoting bone regrowth
 PS Claim 1: Page 12-15; 26pp; English.
 CC Novel human bone morphogenic factor MP52 Arg (W12770) is a growth
 factor that induces formation of cartilage from undifferentiated
 mesenchymal cells and which stimulates the differentiation and
 maturation of osteoblasts. It is effective for treating/preventing
 bone diseases caused by abnormal bone metabolism such as
 osteoporosis. It also accelerates the healing of bone fractures,
 and is useful for orthopaedic reconstruction, bone transplantation,
 and dental therapeutics because of its bone morphogenetic activity.
 CC It is also effective for preventing/treating cartilage, skin,
 connective tissue, mucous membrane, teeth and epithelial disorders.
 CC Recombinant Mp52 Arg can be produced in host (e.g. CHO) cells
 CC utilising an isolated DNA sequence (T59729) in plasmid pMS599.
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEFTVIGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60
 Db 1 MRLPKLLTFLWYLAWLDEFTVIGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60
 QY 61 GGHSGGGATNANARAKGTTGTLTPKDKPKLPPRPGGPEPKGHPPTQRTAAR 120

Db 61 GGHSGGGATNANARAKGTTGTLTPKDKPKLPPRPGGPEPKGHPPTQRTAAR 120
 QY 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPIPHYMLSLYRTL 180
 Db 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPIPHYMLSLYRTL 180
 QY 181 SDADRKGNSVYKLEAGLANITTSIDKQDDRGVVRKQRYVFDISALEKDLGLGAEIR 240
 Db 181 SDADRKGNSVYKLEAGLANITTSIDKQDDRGVVRKQRYVFDISALEKDLGLGAEIR 240
 QY 241 ILRKKPSDTAKPAAPGGGAAQLKLSSCPGROPASLLDVRVPCGLDGSGEVEFDIWLK 300
 Db 241 ILRKKPSDTAKPAAPGGGAAQLKLSSCPGROPASLLDVRVPCGLDGSGEVEFDIWLK 300
 QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360
 Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360
 QY 361 RSGQDDKTVYELFSQRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420
 Db 361 RSGQDDKTVYELFSQRRKRRAPLATROGKRPSKNLKARCSKALHVNFKDMGWDWIIA 420
 QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480
 Db 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480
 QY 481 SANNVYKQYEDMVVESCGR 501
 Db 481 SANNVYKQYEDMVVESCGR 501

RESULT 3
 ID W01799 standard; Protein; 501 AA.
 AC W01799:
 DT 15-OCT-1997 (first entry)
 DE Human MP52 protein.
 KW Human; MP52; transforming growth factor; TGF; beta; medicament;
 KW treatment; prevention; nervous system; disease; neuropathology;
 KW ageing.
 OS Homo sapiens.
 PN DE19525416-Al.
 PD 16-JAN-1997.
 PF 12-JUL-1995; 025416.
 PR 12-JUL-1995; DE-025416.
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
 PI Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K;
 DR WPI: 97-078343/08.
 DR N-PSDB; T59405.
 PT Medicaments contg. protein MP52 - useful for treating neurological
 disorders
 PS Claim 2: Pages 12-14; 21pp; German.
 CC The present sequence is the human Mp52 protein, which is
 described in WO 9316099 and 9504819 as a member of the human
 transforming growth factor beta superfamily. Active MP52 can be
 used in a medicament to treat and prevent nervous system diseases,
 and/or to treat neuropathological conditions caused by nervous
 system ageing.
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEFTVIGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60
 Db 1 MRLPKLLTFLWYLAWLDEFTVIGAPDLGQRPQGTPLGLAKAEKRRPLARNVFRP 60
 QY 61 GGHSGGGATNANARAKGTTGTLTPKDKPKLPPRPGGPEPKGHPPTQRTAAR 120
 Db 61 GGHSGGGATNANARAKGTTGTLTPKDKPKLPPRPGGPEPKGHPPTQRTAAR 120

QY 121 TVTPKGOLPGKAPPKAGSVSSFLKKAREPGPREPEPPPTTPHEYMLSYRTL 180
DB 121 TVTPKGOLPGKAPPKAGSVSSFLKKAREPGPREPEPPPTTPHEYMLSYRTL 180
QY 181 SDADRKGNSSVKLEAGLANITTSFIDKGODDGRGPPVVRKQRYVFDISALEKDGLLGAEIR 240
DB 181 SDADRKGNSSVKLEAGLANITTSFIDKGODDGRGPPVVRKQRYVFDISALEKDGLLGAEIR 240
QY 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300
DB 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300
QY 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360
DB 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360
QY 361 RSGQDDKTVEYLFSSORRRRAPLQTRQGRPSKNLKAARCSKALHVNFKDGMDDWIIA 420
DB 361 RSGQDDKTVEYLFSSORRRRAPLQTRQGRPSKNLKAARCSKALHVNFKDGMDDWIIA 420
QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLNMNDPESTPPTCCVPTRLSPISILFID 480
DB 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLNMNDPESTPPTCCVPTRLSPISILFID 480
QY 481 SANVVYKQYEDMVVESCGR 501
DB 481 SANVVYKQYEDMVVESCGR 501

RESULT 4

W1900
ID W1900 standard; Protein; 501 AA.
AC W1900;
DT 28-OCT-1997 (first entry)
DE Human high mol. wt. protein MP52, a growth/differentiation factor.
KW Growth factor; differentiation; bone induction; osteoporosis; teeth;
KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
KW wound healing; regeneration; skeletal disorder; fracture; dimer.
OS Homo sapiens.
PN WO9704095-A1.
PD 06-FEB-1997.
PR 24-JUL-1996; J02065.
PR 24-JUL-1995; JP-218022.
PA (FARH) HOECHST JAPAN LTD.
PI (FARH) HOECHST PHARM & CHEM KK.
PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
DR WPI; 97-132636/12.
DR N-PSDB; T61412.
PT High molecular weight human MP52 growth or differentiation factor -
PT promotes bone induction, is useful for treatment and prevention of
PT bone disease
PS Claim 1; Page 12-16; 25pp; Japanese.
CC W1900 is a high mol. wt. form of a human growth/differentiation
CC factor MP52. MP52 promotes bone induction and is useful for plastic
CC reconstructive surgery, cosmetic facial treatment, bone transplantation
CC and tooth implantation. It is also useful for the treatment and
CC prevention of disorders of bone formation, bone, cartilage, joint tissue,
CC skin, mucous membranes, nails or teeth; for wound treatment and tissue
CC regeneration; and for the treatment of skeletal disorders and fractures.
CC Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.6e-191;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPQGTGRLAKAEKERPPPLARNVFRP 60
DB 1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPQGTGRLAKAEKERPPPLARNVFRP 60
QY 61 GGHSGGGATNANARAGGTGTGGLTQPKDEPKKLLPPRGPGPEPKPGHPPTQRTAR 120

DB 61 GGHSGGGATNANARAGGTGTGGLTQPKDEPKKLLPPRGPGPEPKPGHPPTQRTAR 120
QY 121 TVTPKGOLPGKAPPKAGSVSSFLKKAREPGPREPEPPPTTPHEYMLSYRTL 180
DB 121 TVTPKGOLPGKAPPKAGSVSSFLKKAREPGPREPEPPPTTPHEYMLSYRTL 180
QY 181 SDADRKGNSSVKLEAGLANITTSFIDKGODDGRGPPVVRKQRYVFDISALEKDGLLGAEIR 240
DB 181 SDADRKGNSSVKLEAGLANITTSFIDKGODDGRGPPVVRKQRYVFDISALEKDGLLGAEIR 240
QY 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300
DB 241 ILRKPSTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300
QY 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360
DB 301 RNFKNQAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKRDLEFNEIKA 360
QY 361 RSGQDDKTVEYLFSSORRRRAPLQTRQGRPSKNLKAARCSKALHVNFKDGMDDWIIA 420
DB 361 RSGQDDKTVEYLFSSORRRRAPLQTRQGRPSKNLKAARCSKALHVNFKDGMDDWIIA 420
QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLNMNDPESTPPTCCVPTRLSPISILFID 480
DB 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLNMNDPESTPPTCCVPTRLSPISILFID 480
QY 481 SANVVYKQYEDMVVESCGR 501
DB 481 SANVVYKQYEDMVVESCGR 501

RESULT 5

W19210
ID W19210 standard; Protein; 501 AA.
AC W19210;
DT 04-MAR-1998 (first entry)
DE Human TGF-beta protein MP52.
KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;
KW cartilage; bone inducing activity; inhibit; bone resorption.
OS Homo sapiens.
PN DE19548476-A1.
PD 26-JUN-1997.
PR 22-DEC-1995; 048476.
PR 22-DEC-1995; DE-048476.
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PI Bechtold R, Hotten G, Paulista M, Pohl J, Hoetten G;
DR WPI; 97-333931/31.
DR N-PSDB; T69695.
PT Compound containing protein from TGF-beta superfamily - has bone
PT and/or cartilage inducing activity, useful in treatment of, e.g.
PT osteoporosis, bone damage, Paget's disease and osteoarthritis
PS Claim 3; Page 9; 10pp; German.
CC This sequence is the human transforming growth factor (TGF)-beta protein
CC designated MP52. MP52 can be used in a compound of formula (I):
CC A-X(1-20)-B(1-20) (I): A = protein, or fragment, of the TGF-beta
CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);
CC B = 1 or more substituent groups with an affinity to the extracellular
CC matrix, cellular components of bone and/or cartilage and/or to a
CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer
CC groups. The compound may be used to inhibit bone resorption, prevent or
CC treat bone or cartilage related disorders, including osteoporosis,
CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthritis and
CC to treat bone or cartilage damage caused by wounding or overloading.
CC Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.6e-191;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPQGTGRLAKAEKERPPPLARNVFRP 60
DB 1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPQGTGRLAKAEKERPPPLARNVFRP 60

Query Match 100.0%; Score 2673; DB 1: Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPPPLARNVFRP 60
 |||||
 DB 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPPPLARNVFRP 60

QY 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVPPGGPEPKPGHPPTQROTAR 120
 |||||
 DB 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVPPGGPEPKPGHPPTQROTAR 120

QY 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPTTPHEYMLSLYRTL 180
 |||||
 DB 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPTTPHEYMLSLYRTL 180

QY 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVFDISALEKDGLLGAELR 240
 |||||
 DB 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVFDISALEKDGLLGAELR 240

QY 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPGLDGSGWEVFDIWKLF 300
 |||||
 DB 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPGLDGSGWEVFDIWKLF 300

QY 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360
 |||||
 DB 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360

QY 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420
 |||||
 DB 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420

QY 421 PLEYEAFHCEGLCEPFLRSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480
 |||||
 DB 421 PLEYEAFHCEGLCEPFLRSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480

QY 481 SANNVYKQYEDMVVESCGR 501
 |||||
 DB 481 SANNVYKQYEDMVVESCGR 501

RESULT 8
 W44868
 ID W44868 standard; protein; 501 AA.
 AC W44868.
 DT 24-SEP-1998 (first entry)
 DE TGF-beta superfamily subunit.
 KW TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;
 KW bone replacement; cartilage; bone; fracture.
 OS Synthetic.
 PN DE19647853-A1.
 PD 20-MAY-1998.
 PF 19-NOV-1996; 047853.
 PR 19-NOV-1996; DE-047853.
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 PA (GERO-) GERONTOCARE.
 PA GMBH BIOMATERIALS & MEDICAL.
 PI Heide H, Pabst J, Paulista M, Pohl J;
 DR WPI; 98-287890/26.
 PT Bioactive implant material for bone replacement - comprising
 PT osteogenic calcium phosphate matrix coated with protein
 PS Claim 3; Page 8-10; 12pp; German.
 CC The TGF-beta superfamily subunit can be used together with a calcium
 CC phosphate matrix to produce a bioactive implant material for bone
 CC replacement. The implant has cartilage and/or bone-forming activity and
 CC can be used for local treatment of cartilage and/or bone diseases or
 CC damage caused by trauma, surgery, degeneration or overloading. The
 CC implant can also be used for the treatment of bone defects, e.g.
 CC parodontosis or fractures and in cosmetic and plastic surgery for fixing
 CC mobile bones.
 SQ Sequence 501 AA;

Query Match 100.0%; Score 2673; DB 1: Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPPPLARNVFRP 60
 |||||
 DB 1 MRLPKLLTFLWYLAWLDEEICTVLGAPDLGQRPQGTGRLGAKAEKERPPPLARNVFRP 60

QY 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVPPGGPEPKPGHPPTQROTAR 120
 |||||
 DB 61 GHSYGGGATNANARAKGGTGTGGLTQPKKDEPKKLPVPPGGPEPKPGHPPTQROTAR 120

QY 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPTTPHEYMLSLYRTL 180
 |||||
 DB 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPREPKEFRPPPTTPHEYMLSLYRTL 180

QY 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVFDISALEKDGLLGAELR 240
 |||||
 DB 181 SDADRKGNSSVKLEAGLANTITSFIDKGDDRGVVRKQRYVFDISALEKDGLLGAELR 240

QY 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPGLDGSGWEVFDIWKLF 300
 |||||
 DB 241 ILRKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDVRSVPGLDGSGWEVFDIWKLF 300

QY 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360
 |||||
 DB 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360

QY 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420
 |||||
 DB 361 RSGDDKTVEYELFSQRRKRRAPLATROGKRPSKNLKAARCSKALHVNFKDMGDDWIIA 420

QY 421 PLEYEAFHCEGLCEPFLRSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480
 |||||
 DB 421 PLEYEAFHCEGLCEPFLRSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480

QY 481 SANNVYKQYEDMVVESCGR 501
 |||||
 DB 481 SANNVYKQYEDMVVESCGR 501

RESULT 9
 R95635
 ID R95635 standard; protein; 501 AA.
 AC R95635;
 DT 25-OCT-1996 (first entry)
 DE Cartilage-derived morphogenetic protein-1.
 KW Human; cartilage-derived morphogenetic protein-1; CDMP-1;
 KW articular cartilage; chondrogenic; vulnary; implantation;
 KW chondromalacia; osteoarthritis; therapy; joint repair.
 OS Homo sapiens.
 FH Key
 FH Location/Qualifiers
 FT peptide 2..19
 FT /note= "Signal peptide"
 FT region 2..377
 FT /note= "Pro-region"
 FT modified_site 189..191
 FT /note= "N-glycosylation site"
 FT cleavage_site 378..381
 FT /note= "Proteolytic processing site"
 FT domain 382..501
 FT /note= "Mature C-terminal domain"
 FT peptide 388..400
 FT /note= "Antigen (R95642) used to raise antibodies"
 FT peptide 417..447
 FT /note= "Highly conserved consensus motif (R95641)"
 PN W09614335-A1.
 PD 17-MAY-1996.
 PF 07-NOV-1994; U12814.
 PR 07-NOV-1994; WO-U12814.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Chang SC, Luyten FP, Moos M;
 DR WPI; 96-251714/25.

DR N-PSDB: T31601.
PT New purified cartilage extracts and proteins - used to stimulate the
PT development and repair of cartilage in vivo.
PS Claim 1; Fig 1; 34pp; English.
CC The sequence represents human articular cartilage-derived
CC morphogenetic protein-1 (CDMP-1). The protein contains a putative
CC transmembrane signal peptide, a pro-region, a typical proteolytic
CC cleavage site, and a C-terminal domain containing 7 highly
CC conserved Cys residues characteristic of the transforming growth
CC factor-beta gene family. A single N-glycosylation site is located
CC in the pro-region. A 13-amino-acid peptide (R95642) has been used
CC to raise rabbit polyclonal antibodies for screening of tissues for
CC CDMP-1 expression. A consensus highly conserved motif in CDMP
CC proteins (R95641) is present in the C-terminal domain. CDMP-1 is
CC present in a purified cartilage extract (claimed) which stimulates
CC local cartilage formation and repair when combined with a matrix
CC and implanted in a mammal. The protein may be used in therapy of
CC e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or
CC to repair cartilage after reconstructive surgery.
SQ Sequence 501 AA;

Query Match 98.4%; Score 2630; DB 1; Length 501;
Best Local Similarity 98.4%; Pred. No. 2.5e-188;
Matches 493; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRLPKLLTLLWYLAWLDELICTVLGAPDLGQRPQGTPLGAKAEKRPPLARNVFRP 60
DB 1 MRLPKLLTLLWYLAWLDELICTVLGAPDLGQRPQGTPLGAKAEKRPPLARNVFRP 60
QY 61 GHSYGGGATNANARAKGTGTGGTQPKDEPKLPKPPGPGPEKPGHPQTRQATAR 120
DB 61 GHSYGGGATNANARAKGTGTGGTQPKDEPKLPKPPGPGPEKPGHPQTRQATAR 120
QY 121 TVTPKQLPGKAPPKAGSVSPSSFLKKAKEPPPREPEKPPPPITPHEYMLSLYRTL 180
DB 121 TVTPKQLPGKAPPKAGSVSPSSFLKKAKEPPPREPEKPPPPITPHEYMLSLYRTL 180
QY 181 SDADKGGNSVKLEAGLANTITSFIDKQDDRGVPVVRKQRYVDFISALEKDLGLGAE 240
DB 181 SDADKGGNSVKLEAGLANTITSFIDKQDDRGVPVVRKQRYVDFISALEKDLGLGAE 240
QY 241 ILRKPSDTAKPAAGGGRAAQLKSSCPGROPASILLVRSVPGLDGSGWEVDFIWKLF 300
DB 241 ILRKPSDTAKPAAGGGRAAQLKSSCPGROPASILLVRSVPGLDGSGWEVDFIWKLF 300
QY 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360
DB 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360
QY 361 RSQDDKTYEYLFQSRKRRAPLARTQGRKPSKNLKAARCSKALHVNFKDGMWDWIIA 420
DB 361 RSQDDKTYEYLFQSRKRRAPLARTQGRKPSKNLKAARCSKALHVNFKDGMWDWIIA 420
QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPTCCVTRLSPISILFD 480
DB 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPTCCVTRLSPISILFD 480
QY 481 SANVYKQYEDMNVESGCR 501
DB 481 SANVYKQYEDMNVESGCR 501

RESULT 10
ID R60022
AC R60022 standard; Protein: 495 AA.
DT 15-MAR-1995 (first entry)
DE Growth differentiation factor 5.
KW GDF-5; growth differentiation factor 5; diagnostic; therapeutic;
KW detection; treatment; cell proliferative disorders; uterine tissue;
KW skeletal tissue; uterine acoplasm; endometriosis; reagent;
KW suppression; transforming growth factor beta superfamily; TGF beta.

OS Mus musculus.
FH Key Location/Qualifiers
FT modified_site 183
FT /note= "potential glycosylation site"
FT cleavage_site 371..375
FT /note= "putative tetrabasic proteolytic processing
FT site"
FT cleavage_site 384..385
FT /note= "putative tetrabasic proteolytic processing
FT site"
PN W09415949-A.
PD 21-JUL-1994.
PF 12-JAN-1994; U00657.
PI 12-JAN-1993; US-003144.
PA (UXJO) UNIV JOHNS HOPKINS SCHOOL MED.
PR Huynh T, Lee S;
DR WPI: 94-249127/30.
DR N-PSDB: 070010.
PT New growth differentiation factor-5 - used to develop prods. for
PT the detection or treatment of cell proliferative disorders of the
PT uterus or skeletal tissue
PS Claim 1; Fig 1; 79pp; English.
CC R60022 shows the amino acid sequence of Growth differentiation
CC factor 5, which is encoded by 070010. The GDF-5 sequence contains
CC a core of hydrophobic amino acids near the N-terminus, suggestive
CC of signal sequence secretion. The sequence contains all of the
CC highly conserved residues present in other members of the
CC transforming growth factor beta superfamily, including the seven
CC cysteine residues with their characteristic spacing. The prods. of the
CC invention can be used for detection of a cell proliferative disorder
CC of the uterus or skeletal tissue which is associated with GDF-5
CC expression. Antisense sequences of GDF-5 can be used to treat uterine
CC neoplasm, endometriosis, or skeletal disorders (claimed). The prods.
CC can also be used in eg. contraception, in vitro fertilisation or in
CC preventing premature labour.
SQ Sequence 495 AA;

Query Match 89.8%; Score 2400; DB 1; Length 495;
Best Local Similarity 91.2%; Pred. No. 3.2e-171;
Matches 457; Conservative 7; Mismatches 31; Indels 6; Gaps 2;

QY 1 MRLPKLLTLLWYLAWLDELICTVLGAPDLGQRPQGTPLGAKAEKRPPLARNVFRP 60
DB 1 MRLPKLLTLLWYLAWLDELICTVLGAPDLGQRPQGTPLGAKAEKRPPLARNVFRP 60
QY 61 GHSYGGGATNANARAKGTGTGGTQPKDEPKLPKPPGPGPEKPGHPQTRQATAR 120
DB 61 GHSYGGGATNANARAKGTGTGGTQPKDEPKLPKPPGPGPEKPGHPQTRQATAR 120
QY 121 TVTPKQLPGKAPPKAGSVSPSSFLKKAKEPPPREPEKPPPPITPHEYMLSLYRTL 180
DB 121 TVTPKQLPGKAPPKAGSVSPSSFLKKAKEPPPREPEKPPPPITPHEYMLSLYRTL 180
QY 181 SDADKGGNSVKLEAGLANTITSFIDKQDDRGVPVVRKQRYVDFISALEKDLGLGAE 240
DB 181 SDADKGGNSVKLEAGLANTITSFIDKQDDRGVPVVRKQRYVDFISALEKDLGLGAE 240
QY 241 ILRKPSDTAKPAAGGGRAAQLKSSCPGROPASILLVRSVPGLDGSGWEVDFIWKLF 300
DB 241 ILRKPSDTAKPAAGGGRAAQLKSSCPGROPASILLVRSVPGLDGSGWEVDFIWKLF 300
QY 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360
DB 301 RNFKNSAQLCLELEAWERGRAVDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360
QY 361 RSQDDKTYEYLFQSRKRRAPLARTQGRKPSKNLKAARCSKALHVNFKDGMWDWIIA 420
DB 361 RSQDDKTYEYLFQSRKRRAPLARTQGRKPSKNLKAARCSKALHVNFKDGMWDWIIA 420
QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPTCCVTRLSPISILFD 480
DB 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPTCCVTRLSPISILFD 480

QY 481 SANNVYKQYEDMVVSCGCR 501
Db 475 SANNVYKQYEDMVVSCGCR 495

RESULT 11
R40800

ID R40800 standard; Protein; 401 AA.
AC R40800;
DT 11-FEB-1994 (first entry)
DE TGF-beta-like clone MP-52 protein.
KW Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
KW bone; cartilage; tooth; wound repair; immunosuppressor;
KW organ transplant; cosmetic surgery; antibody; diagnosis.
OS Homo sapiens.
PN W09316099-A.
PD 19-AUG-1993.
PF 12-FEB-1992; E00350.
PR 12-FEB-1992; EP-102324.
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PI Hoettgen G. Neidhardt H;
DR WFI; 93-272824/34.
DR N-PSDB; Q47709.
PT New transforming growth factor-beta family proteins and DNA -
PT used in tissue and wound repair, in treatment of bone, cartilage
PT and tooth defects, and antibodies for diagnosis
PS Claim 11; Page 19; 29pp; English.
CC The sequences given in R40800 and R45447 represent fragments of embryo
CC and liver derived human transforming growth factor-beta (TGF-beta)
CC respectively. The full length protein may be used in a pharmaceutical
CC composition for the treatment of various bone, cartilage or tooth
CC defects and in tissue and wound repair processes. These proteins may
CC also be used as immunosuppressors in organ transplants and in cosmetic
CC surgery. Antibodies raised against these proteins may be used for
CC diagnostic purposes.
SQ Sequence 401 AA;

Query Match 79.98; Score 2133; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.9e-151;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 PGGPEPKGHPPTQATARTVTPKGOLPGKAPPKAGSVSPSSFLKKAREPGPPREPKE 160
Db 1 PGGPEPKGHPPTQATARTVTPKGOLPGKAPPKAGSVSPSSFLKKAREPGPPREPKE 60

QY 161 PFRPPPTPHEYMLSLYRTLSDADRGKNGSVKLEAGLANTITSFIDKGDDRGPPVVRKQ 220
Db 61 PFRPPPTPHEYMLSLYRTLSDADRGKNGSVKLEAGLANTITSFIDKGDDRGPPVVRKQ 120

QY 221 RYVFDISALEKDGLLGALRLRKPDSATKAPAPGGGAAQLKSSCPGSRQPASLLDV 280
Db 121 RYVFDISALEKDGLLGALRLRKPDSATKAPAPGGGAAQLKSSCPGSRQPASLLDV 180

QY 281 RSVPLDGSWEVFDIWKLFERNKNSAQLCLELEAWERGRAVDLRLGFGDRAARQVHEKA 340
Db 181 RSVPLDGSWEVFDIWKLFERNKNSAQLCLELEAWERGRAVDLRLGFGDRAARQVHEKA 240

QY 341 LFLVFGRTKKRDLFFNFKARSQDDKTVYELFSQRRKRAPLATROGKRPSKNLKARC 400
Db 241 LFLVFGRTKKRDLFFNFKARSQDDKTVYELFSQRRKRAPLATROGKRPSKNLKARC 300

QY 401 SRKALHNFXDMGWDNDIIAPLEYAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPES 460
Db 301 SRKALHNFXDMGWDNDIIAPLEYAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPES 360

QY 461 TPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501
Db 361 TPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 401

RESULT 12

R95636
ID R95636 standard; Protein; 436 AA.
AC R95636;
DT 25-OCT-1996 (first entry)
DE Cartilage-derived morphogenetic protein-2.
KW Cattle; cartilage-derived morphogenetic protein-2; CDMP-2;
KW articular cartilage; chondrogenic; vulnery; implantation;
KW chondromalacia; osteoarthritis; therapy; joint repair.
OS Bos taurus.
FH Key
FT region
FT 1. .312
FT /note= "Pro-region"
FT modified_site
FT 89. .91
FT /note= "N-glycosylation site"
FT cleavage_site
FT 313. .316
FT /note= "Proteolytic processing site"
FT domain
FT 317. .436
FT /note= "C-terminal mature domain"
FT peptide
FT 352. .382
FT /note= "Consensus conserved motif (R95641)"
PN W09614335-A1.
PD 17-MAY-1996.
PF 07-NOV-1994; U12814.
PR 07-NOV-1994; WO-U12814.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Chang SC, Luyten FP, Moos M;
DR WFI; 96-251714/25.
DR N-PSDB; T31602.
PT New purified cartilage extracts and proteins - used to stimulate the
PT development and repair of cartilage in vivo.
PS Claim 11; Fig 2; 34pp; English.
CC The sequence represents cattle articular cartilage-derived
CC morphogenetic protein-2 (CDMP-2). The N-terminal methionine and
CC signal peptide is missing, but part of the pro-region, a typical
CC proteolytic cleavage site and a C-terminal domain containing 7
CC highly conserved Cys residues characteristic of the transforming
CC growth factor-beta gene family are present. A single N-glycosylation
CC site is located in the pro-region. A consensus highly conserved
CC motif in CDMP proteins (R95641) is present in the C-terminal domain.
CC CDMP-2 is present in a purified cartilage extract (claimed) which
CC stimulates local cartilage formation and repair when combined with a
CC matrix and implanted in a mammal. The protein may be used in therapy
CC of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or
CC to repair cartilage after reconstructive surgery.
SQ Sequence 436 AA;

Query Match 33.9%; Score 905.5; DB 1; Length 436;
Best Local Similarity 42.5%; Pred. No. 5.1e-60;
Matches 206; Conservative 65; Mismatches 109; Indels 105; Gaps 15

QY 67 GGATNANARAKGTGTGGTLPKDKPKLPKPPGPGPKGHPPTQATARTVTPKG 126
Db 7 GSAKGMRTKEGRMPRA-----PRENATAREPLDRQEPPEPQRR----- 51

QY 127 QLPGGKAPKAGSVSPSSFLKKAREPGPPREPKEPPPTPHEYMLSLYRTLSDADRK 186
Db 51 -----PPQQ-----PEAREP-----PGRGLVPHPEYMLSLYRTSYIAEKL 86

QY 187 GGNSSVKLEAGLANTITSFIDKGDDRGPPVVRKQYVFDISAL-EKDGILGALRLRK 244
Db 87 GINASFQSKSANTITSFVDRGLDLSHTPLRRQYLFDFVSLDSKEELVGADVRLFRQ 146

QY 245 KPSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDVRSVPGLDGS---GWVEFDIWKLF 301
Db 147 APAALAPPRA---APLAALPLVAPAAGS-----AEPGPAGAPRPGVEFDVWRGLR 195

QY 302 NFKNSAQLCLELE-AW-ERGRA-----VDLRGLGFDRAARQVHEKALFLV 344
Db 196 P-QPWKQLCLELRAAWGGEFGAAEDEARTPGPOPPPPDLRLSLGFGRRVTPQERALLV 254

QY 345 FGRTKKRDLFFNFKAR-----SGDDKTVYELFSQ 376
Db 345 FGRTKKRDLFFNFKAR-----SGDDKTVYELFSQ 376


```
Db 255 FSRQKTL-FAEMREQLGSAETVVGPGGAGSGPPPPPPPTDAGLWSP--SP 311
QY 377 RKRRAPLATROGKRPKSKLAKRCRKALHVNFKMGWDDWIIAPLEAFCEGLCEFP 436
Db 312 GRRRTAFASRGRKGRKSRKSKPLHVNFKELGWDWIIAPLEAYHCEGVCDFP 371
QY 437 LRSHPLEPTNHAVIQTILMSMDPESTPPTCCVTRLSPISILFIDSANNVYKQYEDMVVE 496
Db 372 LRSHPLEPTNHAIQTILMSMDPGSPFPSCCVTKLTPISILYIDAGNNVYNEYEMVVE 431
QY 497 SCGR 501
Db 432 SCGR 436

RESULT 13
ID R78730
AC R78730 standard; Protein; 321 AA.
DE 30-NOV-1995 (first entry)
KW Human mature VL-1 (BMP-13) encoding sequence.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..201
FT protein 202..321
FT misc_difference 202..321 /label= mature protein
FT misc_difference 220..321 /note= "claimed"
FT /note= "claimed"
FN W09516035-A.
PD 15-JUN-1995.
PF 06-DEC-1994; U14030.
PR 07-DEC-1993; US-164103.
PR 25-MAR-1994; US-217780.
PR 02-NOV-1994; US-333576.
PA (GENY ) GENETICS INST INC.
PA (HARD ) HARVARD COLLEGE.
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
PI WPI; 95-224320/29.
DR N-PSDB; Q96208.
PT Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in compsn. for inducing tendon/ligament-like tissue formation
PS Claim 14; Page 62-64; 84pp; English.
CC BMP-12 related proteins are a subset of the BMP/TGF-beta/Vg-1 family of proteins, including BMP-12 and VL-1. VL-1 is designated BMP-13. Like BMP-12, it is expected that BMP-13, as expressed by mammalian cells such as CHO cells, exists as a heterogeneous popn. of active species of BMP-13 protein with varying N-termini. It is expected that all active species will contain the AA sequence beginning with the 19th Cys residue of the mature protein until the 119th residue of the mature protein or until the stop codon after the 120th residue of the mature protein. Other active species contain additional AA sequence in the N-terminal direction. CC Q96208 is a partial DNA sequence and R78730 is the derived AA sequence of a portion of the 2.5 kb DNA insert of the plasmid CC subclone pGEMJLDC31/2.5, derived from clone lambdaJLDC31.
SQ Sequence 321 AA;

Query Match 28.8%; Score 771; DB 1; Length 321;
Best Local Similarity 51.1%; Pred. No. 3.7e-50;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 217 VRKQYVFYSAL-EKDGILGALRLTRKPSDTAKPAPGGGAAQL--KLSCPSGRQ 273
Db 9 LRQKYLFDVMSLSKEELVGLRLFRQAPS-----APWGPAGPLHVLPCLSL--- 60
QY 274 PASLLDVRSV--PGLDGGWEVFDIWKLFNFKNSAQLCLELE-AW---ERGRA----- 322
Db 60 -PLLLDARTLDPQAGPAGGWEVFDVWQGLRH-QPNKQLCLELRAAWGELDAGEAARAG 117
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QY 322 -----VDLRGLGFDRARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKT----- 369
Db 118 PQQPPPDRLSLGFGRRVPPQERALLVFTSRQKNL-FAEMREQLGSAEAGPGAGAE 176
QY 369 -----VYELFSQ-RRKRRAPLATROGKRPKSKLAKRCRKALHVNFKMGWDD 416
Db 177 GSWPPSPGAPDARFWLSPGRRRRRTAFASRGRKGRKSRKPLHVNFKELGWDW 236
QY 417 WIIAPLEYAFHCEGLCEFPPLRSHLEPTNHAVIQTILMSMDPESTPPTCCVTRLSPIS 476
Db 237 WIIAPLEYAFHCEGVCDFPLRSHLEPTNHAIQTILMSMDPGSTPPSCCVTKLTPISI 296
QY 477 LFIDSANNVYKQYEDMVVESCGR 501
Db 297 LYIDAGNNVYKQYEDMVVESCGR 321
```

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RESULT 14
W26591
ID W26591 standard; Protein; 321 AA.
AC W26591;
DT 21-JAN-1998 (first entry)
DE Human bone morphogenetic protein BMP-13.
KW BMP-13; bone morphogenetic protein; human; tendon; ligament; wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
KW therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..201
FT /label= Sig_peptide 202..321
FT /label= Mat_protein /note= "Claim 5" 218..294
FT /note= "Claim 5"
FN US565882-A.
PD 19-AUG-1997.
PF 07-DEC-1993; 164103.
PR 22-DEC-1994; US-362670.
PR 07-DEC-1993; US-164103.
PR 25-MAR-1994; US-217780.
PR 02-NOV-1994; US-333576.
PA (GENY ) GENETICS INST INC.
PA (HARD ) HARVARD COLLEGE.
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
PI WPI; 97-424270/39.
DR N-PSDB; T90386.
PT Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
PT - useful for tissue healing and repair, treatment of tendonitis, improving fixation of tendons to bone etc
PS Claim 5; Column 57-60; 43pp; English.
CC This polypeptide comprises a novel bone morphogenetic protein, its amino acid sequence was deduced from isolated genomic clone vl-1 and/or ligament tissues involves the administration of a composition containing at least one protein selected from BMP-13, MP52 (see W26590) and BMP-12 (see W26589). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and other defects of traumatic or congenital origin, in cosmetic surgery and to improve fixation of tendons or ligaments to bone. The specified proteins CC can also be used to increase activity of other BMPs e.g. BMP-2 (see W26597).
SQ Sequence 321 AA;
```

```
Query Match 28.8%; Score 771; DB 1; Length 321;
Best Local Similarity 51.1%; Pred. No. 3.7e-50;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 31, 1999, 07:15:21 ; Search time 16.18 seconds
(without alignments)
1905.647 Million cell updates/sec

Title: US-09-297-092-1
Perfect score: 2673
Sequence: 1 MRLPKLLTFLWYLAWLDE.....ANNVYQYEDMVVSCGR 501

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database : SPTREMBL10.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.invertebrate.*
14: sp.unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1433	53.6	324	13	Q9YHW9 gallus gall
2	989	37.0	257	13	O42303 brachydanio
3	844.5	31.6	412	13	O12938 brachydanio
4	567.5	12.6	126	13	O93573 gallus gall
5	455.5	17.0	400	13	O57574 brachydanio
6	444	16.6	361	5	O96504 branchiosto
7	439.5	16.4	400	13	O13107 brachydanio
8	437	16.3	411	13	O93369 brachydanio
9	431	16.1	411	13	O57573 brachydanio
10	428.5	16.0	453	13	P87373 gallus gall
11	422	15.8	386	13	O13109 brachydanio
12	420	15.7	301	5	O97390 crassostrea
13	420	15.7	400	13	Q91703 xenopus lae
14	419	15.7	390	13	Q91597 xenopus lae
15	417	15.6	400	13	O73818 xenopus lae
16	412.5	15.4	391	13	P87380 brachydanio
17	409	15.3	411	13	O13108 brachydanio
18	405.5	15.2	614	5	P91720 drosophila
19	397	14.9	424	13	Q9YGH7 xenopus lae
20	391	14.6	373	13	Q98950 gallus gall
21	390	14.6	421	11	Q921V8 Q921V8 mus musculus
22	385	14.4	373	13	Q90723 gallus gall
23	382.5	14.3	354	13	Q9YGV1 xenopus lae
24	381.5	14.3	313	13	Q91403 Q91403 gallus gall
25	379.5	14.2	443	5	O76851 halocynthia
26	376.5	14.1	424	4	O95393 O95393 homo sapien
27	369.5	13.8	178	5	Q25211 junonia coe
28	363	13.6	67	6	O02783 bos taurus
29	361.5	13.5	191	5	Q26468 schistocerc

ALIGNMENTS

```

RESULT 1
Q9YHW9
ID Q9YHW9 PRELIMINARY; PRT; 324 AA.
AC Q9YHW9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE GROWTH DIFFERENTIATION FACTOR 5 PRECURSOR (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEG BUD;
RA MERINO R., MACIAS D., GANAN Y., ECONOMIDES A.N., WANG X., WU Q.,
RA STAHL N., SAMPATH K.T., VARONA P., HURLE J.M.;
RT "Expression and function of Gdf-5 during digit skeletogenesis in the
RT embryonic chick leg bud.";
RL Dev. Biol. 206:33-45(1999).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF075441; AAD14568.1; -.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 324 324
SQ SEQUENCE . 324 AA; 37206 MW; E2CF56AC CRC32;

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Query Match 53.6%; Score 1433; DB 13; Length 324;
Best Local Similarity 83.7%; Pred. No. 1.1e-112;
Matches 273; Conservative 21; Mismatches 30; Indels 2; Gaps 1;

QY 167 ITPEYMLSYRLTSDADRGKSSVKNLEAGLANTITFDKGDGRGVVVRKORVFDI 226
      |||||
DB 1 ITPEYMLSYRLTSDADRGKSSVKNLEAGLANTITFDKGDGRGVVVRKORVFDI 60

QY 227 SALEKGLLGAELRLRKPKSPDTAKPAAGGQRAAQKLSQSPGASLLDVRSPVGL 286
      |||||
DB 61 SALEKGLLGAELRLRKPKSPDAWK--SHSSGKTSQVKLFSCSTNRQAATLLDSRTVSIT 118

QY 287 DSGSWEVDFDITKLFNPKNSAQICLELEAWERGRAVDLRLGDFDRAARQVHEKALFLVFG 346
      |||||
DB 119 DTPKWEVDFDITKLFNPKNSAQICLELEAWERGRAVDLRLGDFDRAARQVHEKALFLVFG 178

QY 347 RTKRDLFFNEIKARSGQDDKTYEYLFSSORRRERAPLATRQGRKPSKNLKAQSRKALH 406
      |||||
DB 179 RTKRDLFFNEIKARSGQDDKTYEYLFSSORRRERAPLATRQGRKPSKNLKAQSRKALH 238

QY 407 VNFKDMGDDWIIAPLEYEAFHCEGLCEFFLRSHLEPTNHAIVTQTLNMSMDPESTPTCC 466
      |||||
DB 239 VNFKDMGDDWIIAPLEYEAFHCEGLCEFFLRSHLEPTNHAIVTQTLNMSMDPESTPTCC 298

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QY 467 VPTRLSPISILFIDSANNVVKQYED 492
 DB 299 VPTRLSPISILFIDSANNVVKQYEE 324

RESULT 2
 ID 042303 PRELIMINARY: PRT: 257 AA.
 AC 042303;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CONTACT (FRAGMENT).
 GN CONTACT.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97398455.
 RA BRUNEAU S., MOURRAIN P., ROSA F.M.;
 RT "Expression of contact, a new zebrafish DVR member, marks mesenchymal
 RT cell lineages in the developing pectoral fins and head and is
 RT regulated by retinoic acid."
 RL Mech. Dev. 65:163-173(1997).
 CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL: Y12005; CAA72733.1;
 DR PFAM: PF00019; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 DR ZFIN: ZDB-GENE-990415-39; contact.
 KW Glycoprotein.
 FT NON-TER 1
 FT CHAIN 140 257 POTENTIAL.
 SQ SEQUENCE 257 AA; 29787 MW; 6BDDCADC CRC32;

Query Match 37.0%; Score 989; DB 13; Length 257;
 Best Local Similarity 71.6%; Pred. No. 1.5e-75;
 Matches 187; Conservative 25; Mismatches 45; Indels 4; Gaps 2;
 QY 241 ILRKPSDTAKPAAGGAAOLKSSCPGROPASLLDVRSPVGLDGSVEFVDIWLK 300
 DB 1 ILRKHMDSKATFSEG--MAVRLFTCSAGNAVALLOARFDSHSASYEVFVDIWKV 58
 QY 301 RNFKNSAQLCELEAWERGRAYDLRLGLFDRAARQVHEKALFLVFGTRKKRLDFFNEIKA 360
 DB 59 KNFRNTPOLCELDVADHGRLDLRLGLSRAGRTKEKAFVFEVGRTRKKGLFNEIKA 118
 QY 361 RSGQDDKTYEYVLFSSORRRKRAPLATROCKRPSKNLAKRCSKALHVNFKDGMGDDWIIA 420
 DB 119 RSGHDKNTYVYLFQRRMRAPLP--RGKKPKPKQRCNKRQLHVNFKDGMGDDWIIA 176
 QY 421 PLEYAFHCEGLCEPRLSHLEPHTHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480
 DB 177 PLEYAFHCEGLCEPRLSHLEPHTHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 236
 QY 481 SANNVVKQYEDMVVSCGCR 501
 DB 237. SANNVVKQYEDMVVSCGCR 257

RESULT 3
 ID 012938 PRELIMINARY: PRT: 412 AA.
 AC 012938;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DYNAMO PROTEIN PRECURSOR.
 GN DYNAMO.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97231294.
 RA BRUNEAU S., ROSA F.;
 RT "Dynamo, a new zebrafish DVR member of the TGF-beta superfamily is
 RT expressed in the posterior neural tube and is up-regulated by Sonic
 RT hedgehog."
 RL Mech. Dev. 64:199-212(1997).
 CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL: X99769; CAA68102.1;
 DR PFAM: PF00019; TGF-beta; 1.
 DR PFAM: PF00688; TGF-beta; 1.
 DR PROSITE: PS00250; TGF-BETA; 1.
 DR ZFIN: ZDB-GENE-980526-442; dynamo.
 KW Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 293 412 DYNAMO PROTEIN.
 SQ SEQUENCE 412 AA; 47071 MW; 1E5AEEL3 CRC32;

Query Match 31.6%; Score 844.5; DB 13; Length 412;
 Best Local Similarity 50.0%; Pred. No. 3.7e-63;
 Matches 179; Conservative 56; Mismatches 82; Indels 41; Gaps 12;

QY 167 ITPHEMLSLYTLSDADRGKSGSVKLEAGLANTITSFIDKQDD--RGPVVRKQRYVF 224
 DB 73 IEPHYMISIVKTSAAEKLGLNASFFRSKANTISFVDEGQDDHLNSPLWR-QKILF 131
 QY 225 DISAL-EKDGLLGAELRLRK-KPSDTAKPAAGGAAOLKSSCPGROPASLLDVR 282
 DB 132 DVSTLSENVEILGAELRIYTKISGFRASSETGP-----VEIQLLSC---QSHTVLDST 182
 QY 283 VPGLDG--SGWEVFDIWLKFR--NFKNSAQLCELEAW--ERGRAVDLRLGLGFPDRAAR 335
 DB 183 LDLEDAHPKWEVDFVDFEIKERQHHSHGNRFLCUELRATLDPNPEREIDQLVGFHHRGP 242
 QY 336 VHEKALFLVFGTRKKRLDFFNEIKARS---GQD-----DKTVYELFSQRKRKRAP 383
 DB 243 QLKRAILVFTRSKQSLFYEKREKIKLWGLDSTGKRRSHSKT-----RSRRTA 294
 QY 384 LATROCKRPSKNLAKRCSKALHVNFKDGMGDDWIIAFLVFEAFHCEGLCEPRLSHLEP 443
 DB 295 LPNRHGKRGHKKSRCSKSKPLHVNFKDGMGDDWIIAFLVFEAFHCEGLCEPRLSHLEP 354
 QY 444 TNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 501
 DB 355 TNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVVKQYEDMVVSCGCR 412

RESULT 4
 ID 093573 PRELIMINARY: PRT: 126 AA.
 AC 093573;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
 GN GDF6/7.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LEE K.J., MENDELSON M., JESSELL T.M.;
 RT "Neuronal patterning by BMPs: A requirement for GDF7 in the
 RT generation of a discrete class of commissural interneurons in the
 RT mouse spinal cord."
 RL Genes Dev. 0:0-0(1998).
 CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DB EMBL: AF089086; AAC97113.1; --

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DR PFAM; pf00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 126 AA; 14265 MW; 612DDD07 CRC32;

Query Match 21.2%; Score 567.5; DB 13; Length 126;
Best Local Similarity 79.4%; Pred. No. 1.5e-40;
Matches 100; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 377 RRRRARPLATPQGR-PSKNLKA RCSRKALHVNPKDMGWDWIIAPLEYEAFHCEGLCEP 435
      ||||| :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 RRRKRTTAA RSGRGHGKKA KTRCSRKRPLHVNFKELGWDDWIIAPLDYEAYHCEGVCF 60

QY 436 PLRSHLEPTNHAVTQTLNMSMDPESTPTCCVPTRLSPISILFIDSANNVYVKQYEDMVV 495
      ||||| :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 PLRSHLEPTNHAIQTTLNMSMDPESTPSCCVPKSLSPISILYIDSGNNVYVKQYEDMVV 120

QY 496 ESCGCR 501
      |||||
Db 121 ETGCCR 126

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RESULT 5
057574 ID O57574 PRELIMINARY; PRT; 400 AA.
057574 AC O57574;
01-JUN-1998 (T-EMBLrel. 06, Created)
01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
DE BONE GENETIC PROTEIN 4.
DE 2BMP-4 OR BMP4.
OS Brachydanio rerio (zebrafish) (Zebra danio).
GC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Rasbora; Rasbora; Danio.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-WHOLE EMBRYO;
RX MEDLINE: 97231284.
RA NIKAIKO M., TADA M., SAJI T., UENO N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE: 97447702.
RX HWANG S.P., TSOU M.F., LIN Y.C., LIU C.H.;
RA "The zebrafish BMP4 gene: sequence analysis and expression pattern
RT during embryonic development.";
RL DNA Cell Biol. 16:1003-1011(1997).
[3]
RN SEQUENCE FROM N.A.
RP HWANG S.P., TSOU M.F., LIN Y.C., LIU C.H.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR ENBL; D49972; BAA24407.1; -.
DR EMBL; AF056336; AAC13302.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 400 AA; 45757 MW; 3FB3C146 CRC32;

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Query Match      17.08; Score 455.5; DB 13; Length 400;
Best Local Similarity 32.5%; Pred. No. 1.6e-30;
Matches 123; Conservative 64; Mismatches 111; Indels 81; Gaps 18;
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Qy	209	GQDRGPVVRKQRXVFDSIALEKDGLG--AELRILRKPKSPDT-AKPAAPGGGAQAQLK--	265
		: : : : : : : : : : : : : : : : :	
Dd	122	LQSD-GSQETPLRFVFNLSSTPDELIIETAELRYVRIQQIDDAFSDPTQDGHGLHRINIY	180
		: : : : : : : : : : : : : : : : :	
Qy	265	--LSSCSFGROPASLLDVRSVPGLDGSGWEVDI-----WKLFRNFKNSAQLCGLLEAW	316
		: : : : : : : : : : : : : : : : :	
Dd	181	EVLKAPREGQITQLDTRLVRH-NTSKWSFDVSPAFLRW--OEKRSNHGLAVEVVQM	237
		: : : : : : : : : : : : : : : : :	
Qy	317	ER-----GRAVDLRGLGFDDRAAROVHE-----KALFLVFGRTKKRDUFFNEIKARS	362
		: : : : : : : : : : : : : : : : :	
Dd	238	KRPVPQKGRHV-----RVSRSVHPLPDDEWDQLRPULLVTFGHDGKSHP-	282
		: : : : : : : : : : : : : : : : :	
Qy	363	QODDKTIYEYLFORSRRRAPLATROGKRPSKNLKACSRKALHNFKMDGWDDHIAPL	422
		: : : : : : : : : : : : : : : : :	
Dd	282	-----TRAKRSP--KORGEKRN-----CRRHALYVDFSDVGNDWIIVAPP	322
		: : : : : : : : : : : : : : : : :	
Qy	423	EYAFHCHEGLCEFFLRSHLEPTNHAIVTQLMNSMDPESTPTCCVPTRLSPISILFIDS	482
		: : : : : : : : : : : : : : : : :	
Dd	323	GYQAYYCHGECPPFLADHLNSTNHAIVQTLVNSYN-TNIPKACCVPTELSAISMLYDET	381
		: : : : : : : : : : : : : : : : :	
Qy	483	NNVYKYOEYDMVWSCGCR	501
		: : : : : : : : : : : : : : : : : :	
Dd	382	DRVYLKNYQEMVVECGCR	400
		: : : : : : : : : : : : : : : : :	
 RESULT 6			
ID	096504	PRELIMINARY;	PRT; 361 AA.
AC	096504;		
DT	01-MAY-1999	(TREMBLrel, 10, Created)	
DT	01-MAY-1999	(TREMBLrel, 10, Last sequence update)	
DT	01-MAY-1999	(TREMBLrel, 10, Last annotation update)	
DE	BONE MORPHOGENETIC PROTEIN 2/4.		
GN	AMPHIBMP2/4.		
OS	Brachiostoma floridae (Florida lancelet) (Amphioxus).		
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;		
ON	Branchiostoma.		
RC	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 98401944.		
RA	PANOPULOU G.D., CLARK M.D., HOLLAND L.Z., LEHRACH H., HOLLAND N.D.;		
RT	"AmphibMP2/4, an amphioxus bone morphogenetic protein closely related		
RT	to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights		
RT	into evolution of dorsoventral axis specification.";		
RL	Dev. Dyn. 213:130-139(1998).		
CC	-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.		
DR	EMBL; AF068750; AAC97488.1; .		
DR	PROSITE; PS00250; TGF_BETA; 1.		
KW	Glycoprotein.		
SQ	SEQUENCE 361 AA; 41517 MW; 3C5F7E25 CRC32;		

[illegible]

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Db 241 SRQKR-----ANGRKQR-----RRLKAMCRHSLYVDFSDVGNWDIV 279
QY 420 APLEYFAFCEGLCEPPLSHLEPTNHAVIQTLNMSMDPESTPTCCVPTSLPSILFI 479
Db 280 APGYQAYCHCECPPLADLHNSLNHAIQVLNVSNPVLAIVKACCVPTDLSPLMYL 339
QY 480 DSANNVYQYEDVMVESCGR 501
Db 340 NENDQVLKYNQDMVVEGCGR 361

RESULT 7
O13107 PRELIMINARY; PRT; 400 AA.
AC O13107
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE BMP4.
GN BMP4.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98036031.
RA MARTINEZ-BARBERA J.P., TORRESSON H., DAROCHA S., KRAUSS S.;
RT "Cloning and expression of three members of the zebrafish Bmp family:
RT Bmp2a, Bmp2b and Bmp4."
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; 882231; AAC60285.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 400 AA; 45757 MW; B95AE8FE CRC32;

Query Match 16.4%; Score 439.5; DB 13; Length 400;
Best Local Similarity 31.7%; Pred. No. 3.5e-29;
Matches 120; Conservative 66; Mismatches 112; Indels 81; Gaps 18;

QY 163 RPPP-----ITPHEMLSLYRTLSADNRKGNSSVKLE-----AGLANTITSF-----IDK 208
Db 63 RRPSSHSAVVP-QYLLDLYLQSGEELAEAGAHVSFDYPERSTSRASTVRGPFHHEHLEE 121
QY 209 GDDRGVVRKORYVDFISALEKDGILG-AELRLRKPSDT-AKPAAPGGGAAQLK-- 265
Db 122 LQSD-GSQETPLRFVFNLSIFDELISTADVKRIYRQIDDAFSDPDQDGDHGLHRIY 180
QY 265 --LSSCPGSPASLLDVRSVPLDGSQWVEFDI-----WKLFRNFKNSAOLCILEAW 316
Db 181 EVLKAPREGQLITQLDLRLVRP-NTSKWESFDVSPAVLRWT--QEKRSNHLGAVVQM 237
QY 317 ER-----GRAVDLRLGLFDRARQVHE-----KALFLVGRTKKRLDFNEIKARS 362
Db 238 KRNVPQKGRHA-----RVRSRVHPLNEEDWHDVRLPLVTFGHGDKSHPL----- 282
QY 363 GQDDKTVYELFSQRRKRAPLATQGRKPSKLNKARCSKALHYNEFKDMGWDWIIAPL 422
Db 282 -----TRAKRSP--KQGRKRNR-----CRHAIYVDFSDVGNWDIVAPP 322
QY 423 EYFAFCEGLCEPPLSHLEPTNHAVIQTLNMSMDPESTPTCCVPTSLPSILFIDSA 482
Db 323 GYQAYYCHCECPPLADLHNSLNHAIQVLNVSNTIPKWCCTPTELSAISMVLDYET 381
QY 483 NNVVYQYEDVMVESCGR 501
Db 382 DRVLKYNQDMVVEGCGR 400
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RESULT 8
O93369 PRELIMINARY; PRT; 411 AA.
AC O93369;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2.
GN BMP2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-FW;
RX MEDLINE; 97231284.
RA NIKAIKO M., TADA M., SAKI T., UENO N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning."
RL Mech. Dev. 61:73-88(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-FW;
RX MEDLINE; 98072322.
RA KISHIMOTO Y., LEE K.H., ZON L., HAMMERSCHMIDT M., SCHULTE-MERKER S.;
RT "The molecular nature of zebrafish swirl: BMP2 function is essential
RT during early dorsoventral patterning."
RL Development 124:4457-4466(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-FW;
RX MEDLINE; 98072322.
RA LEE K.H., MARDEN J.J., THOMPSON M.S., MACLENNAN H., KISHIMOTO Y.,
RA PRATT S.J., SCHULTE-MERKER S., HAMMERSCHMIDT M., JOHNSON S.L.,
RA POSTLETHWAITE J.H., BEIER D.C., ZON L.I.;
RT "Cloning and Genetic Mapping of Zebrafish BMP-2."
RL Dev. Genet. 23:0-0(1998).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF072456; AAC25595.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46873 MW; AF0342A5 CRC32;

Query Match 16.3%; Score 437; DB 13; Length 411;
Best Local Similarity 30.7%; Pred. No. 5.9e-29;
Matches 122; Conservative 59; Mismatches 122; Indels 94; Gaps 1;

QY 150 REPGRPPEPKPPPTTPHEMLSLYRTLSADN-----RKGNSSVKLEAGLANTI 202
Db 64 RKTPSKSAVVP-----QYMLDLYMHSEDDPNRRPRSTMTGKHVERAASRANTI 114
QY 203 TSFID-----KGODRGVVRKORYVDFISALEKDGILG-AELRLRKPSDTAK 251
Db 115 RSFHHEAFELALLSGK-----TQQFFNLSTIPGELISAAELRIFR---DQVLG 164
QY 252 PAAPGGGAAQL-----KLSSCPGSPASLLDVRSVPLDGSQWVEFDIWLFRNFKNSA 307
Db 165 DASTSGFHRINIYEVFRPALAPKEPLRLDLRLVQD-SHTRWESFDVGSVAWARWES 223
QY 308 Q-----LCLEL-----EAWERGRAVDLRLGLFDRARQVH-----EKALFLVFG 346
Db 224 QHNHGLLVLEVLHPKXESVSEAESNRKRV-----RVSRSLHAEDESWAQAARPLVTV- 277
QY 347 RTKKRDLFNEIKARSGODDKTVYELFSQRRKRAPLATQGRKPSK--NLKARCSKA 404
Db 277 -----SHDGGGTAV-----LHNSREKQV-----RGOKPRKHHHNSNCRHHA 315
QY 405 LHVNFKDMGWDWIIAPLEYFAFCEGLCEPPLSHLEPTNHAVIQTLNMSMDPESTPT 464
Db 316 LYVDFSDVGNWDIVAPPYHAFYCHGCEPPLDHLNHNHAIQVLNVSNTIPKVA 374
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RP SEQUENCE FROM N.A.
RX MEDLINE; 98036031.
RA MARTINEZ-BARBERA J.P., TORESSON H., DAROCHA S., KRAUSS S.;
RT "Cloning and expression of three members of the zebrafish Bmp family:
RL Bmp2a, Bmp2b and Bmp4."
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; U82233; AAC60287.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 386 AA; 43374 MW; 6BA60D2F CRC32;

Query Match 15.8%; Score 422; DB 13; Length 386;
Best Local Similarity 32.3%; Pred. No. 9.8e-28;
Matches 120; Conservative 63; Mismatches 117; Indels 72; Gaps 18;

QY 163 RPPITP---HEYMLSLYRTLS-DADR-----KGNSSVKLEAGLANITSF-IDK 208
DB 54 RPTPTSAVVPQMLDLYSAHNSAQVSRPRAHLGKGSERS-----ASRANTIRSFHDE 109

QY 209 GODD--RGVVRKQRYVFDISALEKDLL-GAELRLIRKKPSDTAKPAAPGGGAAQLKL 265
DB 110 STEDPSSSVRTQRFLENLTSPDELYTSADVRFREQIVSSLNNSAGFHRINVHEI 169

QY 266 SSCPQG--ROPAS-LDVRSPGLDGSWEVFDIWLFRNFKNSAQLCLELAWERGRAV 322
DB 170 IR-PSGSLQEPITRLDLTLVQH-SLSKWSFQVTPAVLKWTTDGH-----NHGILV 220

QY 323 DLRLGLFD-----RAARQVHE-----KALFVFGRTKKRDLFENEIKARSGQDDKTIV 369
DB 221 EISHPDQSRKHVRSRSLHNNEDTWSQMRPLLVTSYHDKGNLYHS-----268

QY 370 YEYLFQSRKRRAPLATRQKRPKNLKAQSRKALHVNFKDMGWDWIIAPLEYEAFHC 429
DB 268 -----REKRA-----RNNKQKHH-KANCRHSLYVDFSDVGNWDVIAVPGTHAFYC 315

QY 430 EGLCEPPLRSHLEPTNHAIVQTLNMSMDPEPTPTCCVPTRLSPISILFIDSANNVYKQ 489
DB 316 QGECPPPLADHLNSTNAMVQTLNVSN-SNIPRACCVPTDLSPVSLYLDVEYERVLKN 374

QY 490 YEDMVVSCGCR 501
DB 375 YQDMVVEGCGCR 386

RESULT 12
O97390 PRELIMINARY; PRT; 301 AA.
AC O97390;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE MGDF PRECURSOR.
GN MGDF.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreidae; Crassostrea.
RN [1]
RP SEQUENCE FROM N.A.
RA Lelong C., Mathieu M., Favrel P.;
RT "Structure and expression of mgdf, a new member of the TGF-beta
RT superfamily in Crassostrea gigas (Mollusca Bivalvia).";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AJ130967; CAA10268.1; -.
DR PROSITE; PS00250; TGF-BETA; 1.
DR Signal; Glycoprotein.
KW SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 301 MGDF PRECURSOR.
SQ SEQUENCE 301 AA; 34723 MW; B3B3E804 CRC32;

Query Match 15.7%; Score 420; DB 5; Length 301;
Best Local Similarity 33.9%; Pred. No. 1.1e-27;
Matches 106; Conservative 44; Mismatches 107; Indels 56; Gaps 10;

QY 222 YVFDISALE-KDGLGALRLIRKKPSDTAKPAAPGGGAAQLKLSGSGRQPAS----277
DB 12 FYFNVSIPVESLTGAELRLFDONNET----NPVGNRKQFRHKIETHEVLQPTANSE 67

QY 277 ----LLDVRSPGLDGSWEVFDIWLFRNFKNSAQLCLELAWERGRAVDLRLGLFD--331
DB 58 AITRLDVRHVGG-KNSWESFDIHPAVLKWKKNTL-----NHGLKRVVLSEFNK 117

QY 331 -----RAARQV-----HEKALELVF-----GRKKRDLFFNEIKARSGQDDKT 368
DB 118 PSTDSVKHVRRLRDVESVEAWHERPLLVTTDDNRSRTKTRATSDKKVKKKKRKNK- 177

QY 369 VYEYLFQSRKRRAPLATRQKRPKNLKAQSRKALHVNFKDMGWDWIIAPLEYEAFH 428
DB 177 -----NKRKNRK--KNRKNKTKRKYNNQCRKELNVDFKAVGWNDFWIFAPPGYNAY 228

QY 429 CEGLCFEPPLRSHLEPTNHAIVQTLNMSMDPEPTPTCCVPTRLSPISILFIDSANNVYK 488
DB 229 CDGSHWYFDHNMVTHNAIVQDLVNSIDPRAAPKPCCVPTLSLSTLYTIDHGAVALK 288

QY 489 QYEDMVVSCGCR 501
DB 289 YQDMVVEGCGCR 301

RESULT 13
O91703 PRELIMINARY; PRT; 400 AA.
AC O91703;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PROTEIN 4.
GN BMP-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA SMITH J.C.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE; 93048819.
RA DALE L., HOWES G., PRICE B.M., SMITH J.C.;
RT "Bone morphogenetic protein 4: a ventralizing factor in early Xenopus
RT development."
RL Development 115:573-585(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA METZ A., KNOEHEL S., BUECHLER P., KOESTER M., KNOEHEL W.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; X64538; CAA45836.1; -.
DR EMBL; AJ005076; CAA06333.1; -.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 400 AA; 45778 MW; 74ED45E8 CRC32;

Query Match 15.7%; Score 420; DB 13; Length 400;
Best Local Similarity 31.3%; Pred. No. 1.5e-27;
Matches 116; Conservative 58; Mismatches 127; Indels 70; Gaps 15;

```


Db 331 GDCPFPLADHLNSTNHAIQTLVNSVN-ASIPKACCVPTLSAISMLYLDYDKVVLKNY 389
QY 491 EDMVESCGR 501
Db :|||||
390 QEMVEGCGCR 400

Search completed: October 31, 1999, 07:37:34
Job time: 1333 sec

OM protein - protein search, using sw model
 Run on: October 29, 1999, 10:19:18 ; Search time 11.66 seconds
 (without alignments)
 1214.615 Million cell updates/sec

Title: US-09-297-092-1
 Perfect score: 2673
 Sequence: 1 MRLPKLLTLLWLAWLDE.....ANNVYQYEDVNVESGCGR 501

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2630	98.4	501	1	GDF5_HUMAN
2	2400	88.8	495	1	GDF5_MOUSE
3	905.5	33.9	436	1	GDF6_BOVIN
4	573	21.4	125	1	GDF6_MOUSE
5	510	19.1	151	1	GDF7_MOUSE
6	448	16.8	398	1	BMPA_XENLA
7	443.5	16.6	394	1	BMPA_MOUSE
8	440.5	16.5	396	1	BMP2_HUMAN
9	440.5	16.5	393	1	BMP2_RAT
10	434	16.2	513	1	BMP6_HUMAN
11	433	16.2	396	1	BMP2_DANDA
12	433	16.2	405	1	BMP4_CHICK
13	432	16.2	398	1	BMPB_XENLA
14	428.5	16.0	461	1	DVRL_STRPU
15	428	16.0	452	1	BMP5_MOUSE
16	427.5	16.0	510	1	BMP6_MOUSE
17	427	16.0	593	1	DECA_DROSI
18	426.5	16.0	588	1	DECA_DROME
19	423	15.8	408	1	BMP4_HUMAN
20	422	15.8	401	1	BMP4_XENLA
21	420.5	15.7	454	1	BMP5_HUMAN
22	419	15.7	408	1	BMP6_MOUSE
23	417	15.6	408	1	BMP4_RAT
24	414	15.5	402	1	BMP8_HUMAN
25	408	15.3	408	1	BMP4_DANDA
26	406.5	15.2	353	1	BMP2_CHICK
27	403	15.1	399	1	BMP8_MOUSE
28	402.5	15.1	383	1	UNIV_STRPU
29	401	15.0	621	1	DECA_DROPS
30	397.5	14.9	431	1	BMP7_HUMAN
31	396	14.8	430	1	BMP7_MOUSE
32	381	14.3	426	1	BMP7_XENLA
33	381	14.3	372	1	DECA_TRICA
34	374.5	14.0	427	1	DESLI_CHICK
35	370	13.8	472	1	BMP3_HUMAN
36	367	13.7	360	1	DVRL1_XENLA
37	360.5	13.5	436	1	60A_DROVI
38	358	13.4	355	1	DVRL1_BRARE
39	355.5	13.3	468	1	BMP3_RAT
40	349.5	13.1	399	1	BMP8_MOUSE
41	347	13.0	207	1	BMP6_RAT
42	343.5	12.9	372	1	GDF1_HUMAN
43	341	12.8	455	1	60A_DROME

44 328 12.3 476 1 BM3B_MOUSE P97737 mus musculu
 45 316.5 11.8 476 1 BM3B_RAT P55108 rattus norv

ALIGNMENTS

RESULT 1
 GDF5_HUMAN
 ID GDF5_HUMAN STANDARD; PRT: 501 AA.
 AC P43026;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5) (CARTILAGE-DERIVED
 DE MORPHOGENETIC PROTEIN 1) (CDMP-1).
 DE GDF5 OR CDMP1.
 GN OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX HOETTEN G., NEIDHARDT H., JACOBOWSKY B., POHL J.;
 RA "Cloning and expression of recombinant human growth/differentiation
 RT factor 5."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 204:646-652(1994).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ARTICULAR CARTILAGE;
 RX CHANG S., HOANG B., THOMAS J.T., VUKICEVIC S., LUYTEN F.P.,
 RA RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.;
 RT "Cartilage-derived morphogenetic proteins. New members of the
 RT transforming growth factor-beta superfamily predominantly expressed
 RT in long bones during human embryonic development."
 RL J. BIOL. CHEM. 269:28227-28234(1994).
 CC -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING
 CC HUMAN EMBRYONIC DEVELOPMENT.
 CC -!- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC
 CC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF
 CC DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE
 CC RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE
 CC METACARPALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE
 CC PHALANGES ARE ALMOST SQUARE.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC
 CC EMBL; X80915; G671525; -
 CC EMBL; U13660; G600732; -
 CC MIM; 601146; -
 CC MIM; 201250; -
 CC MIM; 200700; -
 CC DR PROSITE; PS00250; TGF_BETA; 1.
 CC DR PFAM; PF00019; TGF-beta; 1.
 CC DR PFAM; PF00688; TGFb_propeptide; 1.
 CC DR HSP; P18075; 1BMP.
 CC DR SIGNAL; GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
 CC SIGNAL 1 ?
 CC FT PROPEP 381
 CC FT CHAIN 501
 CC FT DISULFID 400 466
 CC FT DISULFID 429 498
 CC BY SIMILARITY.

RESULT 3
GDF6_BOVIN
ID GDF6_BOVIN STANDARD: PRT: 436 AA.
AC P5106;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (CARTILAGE-DERIVED
DE MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT).
GN GDF6 OR CDMP2.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ARTICULAR CARTILAGE;
RX MEDLINE; 95050604.
RA CHANG S., HOANG B., THOMAS J.T., VUKICEVIC S., LUYTEN F.P.,
RA RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.;
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed
RT in long bones during human embryonic development.";
RL J. BIOL. CHEM. 269:28227-28234(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL; U13661; G632490;
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
KW GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
FT NON_TER 1
FT PROPEP <1 316 POTENTIAL.
FT CHAIN 317 436 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 335 401 BY SIMILARITY.
FT DISULFID 364 433 BY SIMILARITY.
FT DISULFID 368 435 BY SIMILARITY.
FT DISULFID 400 400 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 27 27 POTENTIAL.
FT CARBOHYD 89 89 POTENTIAL.
SQ SEQUENCE 436 AA; 47873 MW; 4CC83ABC CRC32;

Query Match 33.9%; Score 905.5; DB 1; Length 436;
Best Local Similarity 42.5%; Pred. No. 1 le-45;
Matches 206; Conservative 65; Mismatches 109; Indels 105; Gaps 16;

Qy 67 GGATNANARAKGGTGOTGLTPQKKDEPKLPPRPGGPEPKPGHPQPTQATARTVTPKG 126
Dy 7 GSAGMRTKEGRMPRA-----PRENATAREPLDRQEPPEPQRR----- 51
Qy 127 QLPGKAPPKAGVSPSELLKAKREPGRPEKPEFRPPPTTPHEYMILYRTLSADRK 186
Dy 51 -----PPQQ-----PEAREP-----PGRGPLVPHEYMILYRTYSIAEKL 86
Qy 187 GNSSVKLEAGLANITTSFDKGDDGRPV-VRKORVVEDISAL-EKDGLGAEILRLK 244
Dy 87 GINAFFOSSKSANTITTSFVDRGLDLSHTPLRQKVLFDVSTLSDEELGVDRVLRQ 146
Qy 245 KPSDTAKPAAPGGGAOLKLSGSCPSGROPASLLDVRSPGLDGS---GWEVEFDIWLKLR 301
Dy 147 APAALAPPA---APLAALRLPVAPAGS-----AEPGACAPRGEVEFDVWRGLR 195

QY 302 NFKNSAQLCLELE-AW--ERGRA-----VDLRGLGFDRAARQVHEKALFLV 344
Dy 196 P-OPWKQLCLELELRAAWGEGPGAEDARTPGQPPPPDLRLSLGFGRRVRTPOERALLVV 254
QY 345 FGRTKKRDLFFNEIKAR-----SGQDDKTVYIEYLFQ 376
Dy 255 FRSQSKTL-FAEMREOLGSATEVVGPGGAGSGPPPPPPSGTDPAGLWSP--SP 311
QY 377 RKRRAPLATROGKRKSKNLKARCSKRLAHVNFKMGWDWDWIAPLEYAFHCEGLCEFP 436
Dy 312 GRRRTAFASRHKRGRKSKRLKLVNFVKELGWDWDWIAPLEYAFHCEGVCDFP 371
QY 437 LRSHLEPTNHAIVTOLMNSMDPEPTCCVPTRLSPISILFIDSANNVYVYQYEDMVE 496
Dy 372 LRSHLEPTNHAIVTOLMNSMDPGSTPPSCVPTKLTPI SILYIDAGNNVYVYEEYVE 431
QY 497 SCGR 501
Dy 432 SCGR 436

RESULT 4
GDF6_MOUSE
ID GDF6_MOUSE STANDARD: PRT: 125 AA.
AC P43028;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (FRAGMENT).
GN GDF6 OR GDF-6.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE; 94195427.
RA STORM E.E., HUYNH T.V., COPELAND N.G., JENKINS N.A., KINGSLEY D.M.,
RA LEE S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily.";
RL NATURE 368:639-643(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; U08338; G488464;
DR MGD; MGI:95689; GDF6
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR HSP; P18075; IBMF.
KW GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN.
FT NON_TER 1
FT PROPEP <1 5 POTENTIAL.
FT CHAIN 6 125 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 24 90 BY SIMILARITY.
FT DISULFID 53 122 BY SIMILARITY.
FT DISULFID 57 124 BY SIMILARITY.
FT DISULFID 89 89 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 125 AA; 14373 MW; AEE04314 CRC32;

Query Match 21.4%; Score 573; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 4 le-27;
Matches 99; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

RESULT 7
BMP2_MOUSE
ID BMP2_MOUSE STANDARD; PRT; 394 AA.
AC P21274;
DT 01-MAY-1991 (REL. 18, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94289485.
RA FENG J.Q., HARRIS M.A., GHOSH-CHOUDHURY N., FENG M., MUNDY G.R.,
RA HARRIS S.E.;
RT "Structure and sequence of mouse bone morphogenetic protein-2 gene
(BMP-2): comparison of the structures and promoter regions of BMP-2
and BMP-4 genes.";
RL BIOCHIM. BIOPHYS. ACTA 1218:221-224(1994).
RN [2]
RP SEQUENCE OF 1-351 FROM N.A.
RX MEDLINE; 90228966.
RA DICKINSON M.E., KOBRIN M.S., SILAN C.M., KINGSLEY D.M., JUSTICE M.J.,
RA MILLER D.A., CECI J.D., LOCK L.F., LEE A., BUCHBERG A.M.,
RA SIRACUSA L.D., LYONS K.M., DERYNCK R., HOGAN B.L.M., COPELAND N.G.,
RA JENKINS N.A.;
RT "Chromosomal localization of seven members of the murine TGF-beta
superfamily suggests close linkage to several morphogenetic mutant
loci";
RL GENOMICS 6:505-520(1990).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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RA WOZNEY J.M., ROSEN V., CELESTE A.J., MITSOCK L.M., WHITTERS M.J.,
RT KRIZ R.W., HEWICK R.M., WANG E.A.;
RT "Novel regulators of bone formation: molecular clones and
activities.";
RL SCIENCE 242:1528-1534 (1988).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND
CC COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
CC LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
CC SMALL INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL; M22489; G179502;
CC PIR; B37278; B37278.
CC MIN; 112261;
CC PROSITE; PS00250; TGF-beta; 1.
CC PFAM; PF00019; TGF-beta; 1.
CC PFAM; PF00688; TGF-beta; 1.
CC HSP; P18075; 1BMP.
CC SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
CC
CC FT SIGNAL 1 ?
CC FT PROPEP 1 ?
CC FT CHAIN 283 396
CC FT DISULFID 296 361
CC FT DISULFID 325 393
CC FT DISULFID 329 395
CC FT DISULFID 360 360
CC FT CARBOHYD 135 135
CC FT CARBOHYD 163 163
CC FT CARBOHYD 164 164
CC FT CARBOHYD 200 200
CC SEQUENCE 396 AA; 44702 MW; 182782C0 CRC32;

Query Match 16.5%; Score 440.5; DB 1; Length 396;
Best Local Similarity 30.68; Pred. No. 5.5e-19;
Matches 136; Conservative 61; Mismatches 149; Indels 99; Gaps 19;
Qy 94 PKLPPRPGGPEPPHPPQTRQATRTVTPKGLPGKAPPKAGSVPSFLKKAREPG 153
Db 14 PQVLLGGAAGLVPELG---RRKFAAASSGRPSQ-----PSDEVLSFELRLSMFG 62
Qy 154 PPREPEFRPPPTTPHYMLSLYTLIS-DADRGKGNSSVKLEAGLANTITSF-----ID 207
Db 63 LKQRP-TPSRDAVVP--YMLDLVRRHSQGPSPADHRLERAASRANTVSPHESLE 119
Qy 208 KGQDRGPPVQRVDFDISAL-EDGGLLGAELRLKKPSDT-----A 250
Db 120 ELPEFSGKTR--RFFNLSIPTFEFTSAELQVFEQMDALGNSSFFHRIIYEII 177
Qy 251 KPAAPGGGAAQLKSSPCSGRPASLDVRSVPGDQSGVEFDIWKLFNFKNSAQ-- 309
Db 178 KPAITAN-----SKFPVTR---LLDTRLV-NQNASRSESDVTPAVNRW--TAQGH 221
Qy 309 ----LCLELEWNRGAVDLRGLGFDRAARQVHE-----KALFLVFGTKRKDLFFN 356
Db 222 ANHGFVVEVAHLEEKQGVSKRHV---RISRSLHQDEHSWSQIRPLLVTFGHDGR----- 273
Qy 357 EIKARSGDDTVVTEYLFQSRKKRRAPLATQGRKPSKNLKAACSRKALHVFNDMGWD 416
Db 273 -----GPHUHKREKQAKHKQ-----KRLKSSCKRHPLYVDFSDVGWMD 312
Qy 417 WIIAPLEYAFHCEGLCEFPFLHRSLEPTNHAVIOTLMSMDPESTPTCCVPTLRSPI 476

Db 313 WIVAPPGYHAFYCHGCEPFFPLADHLNSTHAIYQTLVNSVN-SKIPKACCVPTLSAISM 371
Qy 477 LFIDSANNVYKQYEDMVESGCR 501
Db 372 LYLDENEKVVLYKNYQDMVVEGCGCR 396
RESULT 9
BMP2_RAT
ID BMP2_RAT STANDARD; PRT; 393 AA.
AC P49001;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=BONE;
RA FENG J.O., CHEN D., FENG M., HARRIS M.A., MUNDY G.R., HARRIS S.E.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z25868; G397951;
CC PROSITE; PS00250; TGF-beta; 1;
CC PFAM; PF00019; TGF-beta; 1.
CC PFAM; PF00688; TGF-beta; 1.
CC HSP; P18075; 1BMP.
CC SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
CC
CC FT SIGNAL 1 ?
CC FT PROPEP 1 ?
CC FT CHAIN 280 393
CC FT DISULFID 293 358
CC FT DISULFID 322 390
CC FT DISULFID 325 392
CC FT DISULFID 357 357
CC FT CARBOHYD 133 133
CC FT CARBOHYD 161 161
CC FT CARBOHYD 197 197
CC FT CARBOHYD 335 335
CC SEQUENCE 393 AA; 44383 MW; 582689AF CRC32;

Query Match 16.5%; Score 440.5; DB 1; Length 393;
Best Local Similarity 31.7%; Pred. No. 5.5e-19;
Matches 133; Conservative 54; Mismatches 131; Indels 101; Gaps 19;
Qy 137 AGSVPSFLKKAREGPPPREPEPF-----RPPP---ITPHEYMLSLY 177
Db 22 AGLIELGRKKFKAGASRPLSRPSEDLSEFELRLSMFGKQRTPTSKDVVPPYMLDLY 81
Qy 178 RTLSADARKGNSSV-----KLE--AGLANTITSF-----IDKGDDRGPPVQRVDF 225
Db 82 R-----RHSGQCALAPDHLERAASRANTVLSFHHEEAIEELSEMSGKTSR--RFFN 133
Qy 226 ISALEKDGLL-GAELRILRKPSDTAKPAAPGGGAAQLKLS-----SCPSGRQFAS- 277
Db 134 LSSVPTDEFLTSAELQIFREOMGEAL-----GNSSFQHRINIYEIKPATASSKFPVTR 187

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 CC -----
 CC EMBL: AJ001817; E352086; -
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR PFAM; PF00019; TGF-beta; 1.
 DR PFAM; PF00688; TGF-beta; 1.
 DR HSP; P18075; 1BMP.
 KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
 FT SIGNAL 1 2
 FT PROPEP 282
 FT CHAIN 283 396
 FT DISULFID 296 361
 FT DISULFID 325 393
 FT DISULFID 329 395
 FT DISULFID 360 360
 FT CARBOHYD 135 135
 FT CARBOHYD 163 163
 FT CARBOHYD 164 164
 FT CARBOHYD 200 200
 FT CARBOHYD 338 338
 FT SEQUENCE 396 AA; 44646 MW; 8C56358B CRC32;

Query Match 16.2%; Score 433; DB 1; Length 396;
 Best Local Similarity 30.4%; Pred. No. 1.5e-18;
 Matches 128; Conservative 51; Mismatches 132; Indels 110; Gaps 16;

QY 129 PGKAPKAGSVSSFLKKARPGPPREPKEPPPTTPHEYMILSLRTLS-DADRKG 187
 DB 38 PGSSSQSDVLSEFELRLLSMFLGKQRP-TPSRDPVPP--YMLDLYLHSGQPGAPA 94
 QY 188 GNSVKLEAGLANTITSF-----IDKGDDRGPPVWRKQRYVEDISAL-EKDGILGAELEI 241
 DB 95 PGRLEAASLANVTRTFHEESLEELPEMSGKTR--RFFNLTSTIPEFTISAELOV 152
 QY 242 LRKKPSDT-----AKPAPEGGRAGAAQLKSSCPGSPGASLLDVRSPVG 285
 DB 153 FGKHPPEALENNSFFHRIIFELIRPATAN-----SKFPVTR---LLDTRLVT- 199
 QY 286 LDGSGWEVDIWLKFRNFKNSAQLELEAWERGRAVDLRGLGF----- 330
 DB 199 QNASRWESFDV-----TPAVMRTAQGLNHGTVVEVAHPEDSYGASKR 242
 QY 330 -DRAARQVHE-----KALFLVFGRTKKRDLFFNEIKARSGDDKTVVEYLFSSORRR 380
 DB 243 HVRISRLHQDEHSWSQIRPLLVTFCHDGK-----GHPHLHREKR 282
 QY 381 RAPLATRQGRKPKSKNKLKARSKALHVNFKMGDWDWIAPLEYAFHCEGLCEFFLRSH 440
 DB 283 QAKHKOR-----KRLKSSCKRPLXVDFSDGVNDWIVAPPYHAFYCHGCEPPLADH 336
 QY 441 LEPTNHAIVOTLANSMDPESTPTCCVPTLSPISILFSDSANNVYKQYEDWVVECGC 500
 DB 337 LNSTNHAIVOTLVNSVN-SKIPKACCVPTLSAISMLYLDENEKVVLKNYQDMVVEGCGC 395
 QY 501 R 501
 DB 396 R 396

RESULT 12
 BMP4_CHICK
 ID BMP4_CHICK STANDARD; PRT; 405 AA.
 AC Q90752;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).

GN BMP4 OR BMP-4.
 OS GALLUS GALLUS (CHICKEN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEGHORN;
 RA MEDLINE; 94163974.
 RX FRANCIS P.H., RICHARDSON M.K., BRICKELL P.M., TICKLE C.;
 RT "Bone morphogenetic proteins and a signalling pathway that controls
 RT patterning in the developing chick limb.";
 RL DEVELOPMENT 120:209-218(1994)
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL: X75915; G472930; -
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR PFAM; PF00019; TGF-beta; 1.
 DR PFAM; PF00688; TGF-beta; 1.
 DR HSP; P18075; 1BMP.
 KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
 FT SIGNAL 1 19
 FT PROPEP 20 291
 FT CHAIN 292 405
 FT DISULFID 305 370
 FT DISULFID 334 402
 FT DISULFID 338 404
 FT DISULFID 369 369
 FT CARBOHYD 144 144
 FT CARBOHYD 208 208
 FT CARBOHYD 347 347
 FT CARBOHYD 362 362
 FT SEQUENCE 405 AA; 46057 MW; A60C5A50 CRC32;

Query Match 16.2%; Score 433; DB 1; Length 405;
 Best Local Similarity 30.4%; Pred. No. 1.5e-18;
 Matches 123; Conservative 64; Mismatches 153; Indels 64; Gaps 14;

QY 125 KGQFGGRAPKAGSVPSF-----LLKKAREPGPPREPKEPPPTTPHEYMILSLR 178
 DB 39 QGQAGSGRNSAOSHLLRGFTTLLQMGFLRRRPPQPSKSAVIP-----SYMDDLYR 89
 QY 179 TLSDADRKGNSSVKLE-----AGLANTITSFIDRGDDRG--VWRKQRYVFDISALE 230
 DB 90 LOSGEEERSLQEISIQYPERASANTVRSFHEEHLSEVSGPSEAPRIRFVNLSSVP 149
 QY 231 KDELIGA-ELRLRKPSDTAKPAAPGGGAAQLKSSCPGSRQA--SLLDVRSVGLD 287
 DB 150 DNEVISSESLRLYREQVEPSSAAWGERGFHRIYEVMPKPLSERSQAITRLDTRLVHH-N 208
 QY 288 GSGWEVDIWLKFRNFKNSAQ-----LCLELEAWERGRAVDLRGLGFDRARQVHE----- 339
 DB 209 VTRWETFDVSPAVIRKTKDQPNHGLVIEVTHLHOAQTHQGHKVRISRLPGHGGDWAQ 268
 QY 339 -KALFLVFGRTKKRDLFFNEIKARSGDDKTVVEYLFSSORRRRAPLATROCKRKNLK 397
 DB 269 LRPLLVTFCHDGCHAL-----TRRRRSP--KHGCR--KN-K 302
 QY 398 ARCSKALHVNFKMGDWDWIAPLEYAFHCEGLCEFFLRSHLEPTNHAIVOTLVNSMD 457
 DB 303 KNCRRHALYVDFSDGVNDWIVAPPYHAFYCHGDCPPLADHLNSTNHAIVOTLVNSVN 362
 QY 458 PESTPTCCVPTLSPISILFSDSANNVYKQYEDWVVECGCR 501

Db 363 SSIPKACCVPTLSAISMVLYDEYDKVVLKYNQEMVVEGCGCR 405

RESULT 13

BMPB_XENLA
ID BMPB_XENLA STANDARD; PRT; 398 AA.
AC P30884;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DE BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE; 92378616.
RA NISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 186:1487-1495(1992).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; X63425; G64584;
DR PIR; JH0688; JH0688.
DR PROSITE; PS00250; TGF_BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGFb_propeptide; 1.
DR HSP; P18075; IBMP.
KW SIGNAL; GROWTH FACTOR; CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
FT SIGNAL 1
FT PROPEP 1
FT CHAIN 285 398
FT DISULFID 298 363
FT DISULFID 327 395
FT DISULFID 331 397
FT DISULFID 362 362
FT CARBOHYD 137 137
FT CARBOHYD 202 202
FT CARBOHYD 237 237
FT CARBOHYD 340 340
SQ SEQUENCE 398 AA; 45616 MW; E7D1DFBA CRC32;

Query Match 16.2%; Score 432; DB 1; Length 398;
Best Local Similarity 32.1%; Pred. No. 1.7e-18;
Matches 127; Conservative 62; Mismatches 143; Indels 64; Gaps 18;

QY 133 APKAGSVPSFLKAKAREPGPREP---KEPFRPPPTTHPEYMLSLYRTLSDD--ADRGK 187
DB 40 SPQSQQVLDQFELRLNMGFKRRPTGKNVVP-----YMLDLVHLHSAQLADQOG 93
QY 188 GNS---SVKLEAGLANTITSFDKQDDRGPPVVRK---QRYVFDISALEKGLL-GAELR 240
DB 94 SSEVDYHMERASRANTVSRPHSEMEIPESGEKTIQRFFNLSIPDEELVTSSEL 153
QY 241 ILRKPSDTAKAARGGGAOLKL-----SSCPGROP-ASLLDVRSPGLDGGWEVF 294
DB 154 IFREQ---VQEPFKTDGSKLHRINIYDIVKPAASASRGPPVRLDTRLIHH-NESKWSF 209
QY 295 DTKLFRNFKNSAQLCLELAW-----ERGRAVDLRLGLGEDRAARQVH---EKALFLVF 345

Db 210 DVTP-----AITRWIAHKQPNHGVVEVTHLNDNTNPKRHRVIRSLTLDK 256
QY 346 GRTKKRLFFNEIKARSGQDDKTVVEYLFQORRRRAPLATROGKRPSKMLKARCSKAL 405
DB 257 GHWRP-----IRPLLVTFSDHGK---GHALHKRQROA---RHQR--KRLKSSCRHPL 303
QY 406 HVNEKMGWDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHAIVTQTLNMSNDPESTPTC 465
DB 304 YVDFSDGVNDWIVAPPYHAFYCHGCEPPLADHLNSTNHAIVOTLVNSVN-TNIPKAC 362
QY 466 CVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501
DB 363 CVPTLSAISMLYLDENEKVVVKYQDMVVEGCGCR 398

RESULT 14

DVRL_STRPU
ID DVRL_STRPU STANDARD; PRT; 461 AA.
AC P48969;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE DVRL-1 PROTEIN HOMOLOG PRECURSOR.
GN DVRL.
OS STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).
OC EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
OC EUECHINOIDEA; ECHINACEA; ECHINOIDA; STRONGYLOCENTROTIDAE;
OC STRONGYLOCENTROTUS.
RN [1]
SEQUENCE FROM N.A.
RA PONCE M.R., MICOL J.L., DAVIDSON E.H.;
RL SUBMITTED (FEB-1995); TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; Z48313; G673497;
DR PROSITE; PS00250; TGF_BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGFb_propeptide; 1.
DR HSP; P18075; IBMP.
KW GROWTH FACTOR; CYTOKINE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1
FT PROPEP 31 338
FT CHAIN 339 461
FT DISULFID 360 426
FT DISULFID 389 458
FT DISULFID 393 460
FT DISULFID 425 425
FT CARBOHYD 149 149
FT CARBOHYD 402 402
SQ SEQUENCE 461 AA; 51881 MW; 57C7CBA0 CRC32;

Query Match 16.0%; Score 428.5; DB 1; Length 461;
Best Local Similarity 29.7%; Pred. No. 3.2e-18;
Matches 129; Conservative 48; Mismatches 105; Indels 153; Gaps 17;

QY 163 RPPITTHEYML-----SLYRTLSADRGKGNSSVKLEAG----- 198
DB 82 RPSLRGQGNQFOCAQFTWYSYRTLNIDEQSGHPSETPEQPGGLASNAIYNPSSGIGS 141
QY 198 -----LANTITS-----FIDKQDDRGPPVVRKORYVFDISAL-EKDGL 234
DB 142 VMSGTVFNTRYNEQAVSQADTINSLPHYKDAIED-----TEHRYFDIGRIPQETV 196

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 31, 1999, 07:02:15 : Search time 14.26 Seconds
(without alignments)
1407.630 Million cell updates/sec

Title: US-09-297-092-1
Perfect score: 2673
Sequence: 1 MRLPKLLTLLWYLAWLDE.....ANNVYKQYEDMWVESCGR 501

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database : PIR 60.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2673	100.0	501	JC2347	growth/differentia
2	2630	98.4	501	A53452	cartilage-derived
3	2400	89.8	495	S43294	bone morphogenetic
4	905.5	33.9	436	B53452	cartilage-derived
5	573	21.4	125	S43295	bone morphogenetic
6	510	19.1	151	S43296	bone morphogenetic
7	447	16.7	398	JH0687	bone morphogenetic
8	443.5	16.6	394	S43355	bone morphogenetic
9	440.5	16.5	396	BMH02	bone morphogenetic
10	440.5	16.5	393	S37073	bone morphogenetic
11	434	16.2	513	BMH06	bone morphogenetic
12	433	16.2	405	I50608	bone morphogenetic
13	432	16.2	398	JH0688	bone morphogenetic
14	428.5	16.0	461	S52408	bone morphogenetic
15	428	16.0	452	I49542	bone morphogenetic
16	427.5	16.0	510	A54798	Vg-1-related prote
17	426.5	16.0	588	A26158	decapentaplegic pr
18	423	15.8	408	BMH04	bone morphogenetic
19	422	15.8	401	JH0689	bone morphogenetic
20	420.5	15.7	454	BMH05	bone morphogenetic
21	420	15.7	400	A49147	bone morphogenetic
22	419	15.7	420	I49541	bone morphogenetic
23	417	15.6	408	S38343	bone morphogenetic
24	414	15.5	402	A45056	bone morphogenetic
25	409	15.3	408	JH0801	osteoegenic protein
26	408	15.3	408	S58791	bone morphogenetic
27	406.5	15.2	353	I50607	bone morphogenetic
28	397.5	14.9	431	BMH07	bone morphogenetic
29	396	14.8	430	JQ1184	bone morphogenetic
30	381.5	14.3	313	I51284	osteoegenic protein
31	381	14.3	426	JH0690	bone morphogenetic
32	374.5	14.0	427	A40735	TGF beta homolog d
33	370	13.8	472	BMH03	bone morphogenetic
34	367	13.7	360	A29619	Vg1 embryonic grow
35	347	13.0	207	S37618	vgr protein - rat
36	343.5	12.9	372	C39364	GDF-1 embryonic gr
37	341	12.8	455	A43918	TGF-beta-related p
38	322	12.0	351	A34201	bone morphogenetic
39	316.5	11.8	476	JC4646	bone morphogenetic

growth/differentia
bone morphogenetic
bone morphogenetic
bone morphogenetic
transforming growt
GDF-1 embryonic gr
inhibin beta-A cha

ALIGNMENTS

RESULT 1
JC2347
growth/differentiation factor 5 - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Apr-1998
C:Accession: JC2347
R:Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A:Title: Cloning and expression of recombinant human growth/differentiation factor-5.
A:Reference number: JC2347
A:Accession: JC2347
A:Molecule type: DNA
A:Residues: 1-501 <HOE>
C:Genetics:
A:Gene: GDB:BMH9
A:Cross-references: GDB:433948
A:Introns: 211/1
C:Keywords: glycoprotein
F:189/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 100.0%; Score 2673; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 8e-172;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRLPKLLTLLWYLAWLDEFTCTVLGAPDLGCRPGTTPGLAKAEKRPPLARNVFP	60
Db	1	MRLPKLLTLLWYLAWLDEFTCTVLGAPDLGCRPGTTPGLAKAEKRPPLARNVFP	60
Qy	61	GGHSYGGGATNANAKGGTGTGTGTPKDEPKKLPRPGGPPKPGHPPTQATAR	120
Db	61	GGHSYGGGATNANAKGGTGTGTGTPKDEPKKLPRPGGPPKPGHPPTQATAR	120
Qy	121	TVTPKGQLPGGKAPKAGSVSPSSFLKKAREPGPREPPEPPITPHEMYLSLYRTL	180
Db	121	TVTPKGQLPGGKAPKAGSVSPSSFLKKAREPGPREPPEPPITPHEMYLSLYRTL	180
Qy	181	SDADRRKGGNSVYKLEAGLANTITSTFDKGQDDRGVPVVRKQRYVFDISALEKDLGAEUR	240
Db	181	SDADRRKGGNSVYKLEAGLANTITSTFDKGQDDRGVPVVRKQRYVFDISALEKDLGAEUR	240
Qy	241	ILRKPSDTAKPAAPGGGAAAKLSSCSGSGRQASLLDVRSVPGLDGSGWEVDFIWKLF	300
Db	241	ILRKPSDTAKPAAPGGGAAAKLSSCSGSGRQASLLDVRSVPGLDGSGWEVDFIWKLF	300
Qy	301	RNFKNSAQCLLEAWERGRAVDRLGLGPDRAARQVHEKALFLVFGRTKKRDLFFNETKA	360
Db	301	RNFKNSAQCLLEAWERGRAVDRLGLGPDRAARQVHEKALFLVFGRTKKRDLFFNETKA	360
Qy	361	RSQDDKTYVEYLFSSORRRKRAPLATROGKRPSKLNKARCSKALHVNFKDWDWIIA	420
Db	361	RSQDDKTYVEYLFSSORRRKRAPLATROGKRPSKLNKARCSKALHVNFKDWDWIIA	420
Qy	421	PLEYEAHFHCEGCEFFLRSHLEPTNHAVTQTLNMSMDPESTPTCCVPTRLSPISILFID	480
Db	421	PLEYEAHFHCEGCEFFLRSHLEPTNHAVTQTLNMSMDPESTPTCCVPTRLSPISILFID	480
Qy	481	SANNVYKQYEDMWVESCGR 501	
Db	481	SANNVYKQYEDMWVESCGR 501	


```

RESULT 2
A55452
cartilage-derived morphogenetic protein 1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999
C:Accession: A55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth
A:Reference number: A55452; MUID:95050604
A:Accession: A55452
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-501 <CHA>
A:Cross-references: GB:U13660; NID:g600731; PID:g600732
C:Genetics:
A:Gene: GDB:CDMP1
A:Cross-references: GDB:438940

Query Match 98.4%; Score 2630; DB 2; Length 501;
Best Local Similarity 98.4%; Pred. No. 6e-169;
Matches 493; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPQGTTPGLAKAEKERPPPLARNVFP 60
DB 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPQGTTPGLAKAEKERPPPLARNVFP 60
QY 61 GGHSYGGGATNANAKGGTGTGGLTQPKKDEPKKLPVPPGGPKPGHPPTQQTAR 120
DB 61 GGHSYGGGATNANAKGGTGTGGLTQPKKDEPKKLPVPPGGPKPGHPPTQQTAR 120
QY 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTPHEYMLSLYRTL 180
DB 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTPHEYMLSLYRTL 180
QY 181 SDADKRGNSVVKLEAGLANITTSFIDKGDDRGVVRKQRYVFDISALEKDGGLGAE 240
DB 181 SDADKRGNSVVKLEAGLANITTSFIDKGDDRGVVRKQRYVFDISALEKDGGLGAE 240
QY 241 ILRKPSDTAKPAAPGGGAAQKLSGPCSGROPASLLDVRSPGLDGSWEVDIWKLF 300
DB 241 ILRKPSDTAKPAAPGGGAAQKLSGPCSGROPASLLDVRSPGLDGSWEVDIWKLF 300
QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
DB 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
QY 361 RSGQDDKTVYELFSQRKRRAPLATROGKRPKNLKAAROVHEKALFLVFGRTKKRDLFFNEIKA 420
DB 361 RSGQDDKTVYELFSQRKRRAPLATROGKRPKNLKAAROVHEKALFLVFGRTKKRDLFFNEIKA 420
QY 421 PLEYEAFHCEGLCEPFLSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480
DB 421 PLEYEAFHCEGLCEPFLSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480
QY 481 SANNVVYKQYEDMVVESCGR 501
DB 481 SANNVVYKQYEDMVVESCGR 501

RESULT 3
S43294
bone morphogenetic protein-related protein (GDF5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43294
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427
A:Accession: S43294

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <STO>

Query Match 89.8%; Score 2400; DB 2; Length 495;
Best Local Similarity 91.2%; Pred. No. 1.5e-153;
Matches 457; Conservative 7; Mismatches 31; Indels 6; Gaps 2;

QY 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPQGTTPGLAKAEKERPPPLARNVFP 60
DB 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQGTTPGAKPGLTAKAEKERPPPLARNVFP 60
QY 61 GGHSYGGGATNANAKGGTGTGGLTQPKKDEPKKLPVPPGGPKPGHPPTQQTAR 120
DB 61 GGHSYGGGATNANAKGGTGTGGLTQPKKDEPKKLPVPPGGPKPGHPPTQQTAR 120
QY 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTPHEYMLSLYRTL 180
DB 121 TVTPKGQLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTPHEYMLSLYRTL 180
QY 181 SDADKRGNSVVKLEAGLANITTSFIDKGDDRGVVRKQRYVFDISALEKDGGLGAE 240
DB 181 SDADKRGNSVVKLEAGLANITTSFIDKGDDRGVVRKQRYVFDISALEKDGGLGAE 240
QY 241 ILRKPSDTAKPAAPGGGAAQKLSGPCSGROPASLLDVRSPGLDGSWEVDIWKLF 300
DB 241 ILRKPSDTAKPAAPGGGAAQKLSGPCSGROPASLLDVRSPGLDGSWEVDIWKLF 300
QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
DB 301 RNFKNSAQLCLELEAWERGRAVDLRLGLGFDRAAROVHEKALFLVFGRTKKRDLFFNEIKA 360
QY 361 RSGQDDKTVYELFSQRKRRAPLATROGKRPKNLKAAROVHEKALFLVFGRTKKRDLFFNEIKA 420
DB 361 RSGQDDKTVYELFSQRKRRAPLATROGKRPKNLKAAROVHEKALFLVFGRTKKRDLFFNEIKA 420
QY 421 PLEYEAFHCEGLCEPFLSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480
DB 421 PLEYEAFHCEGLCEPFLSHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFID 480
QY 481 SANNVVYKQYEDMVVESCGR 501
DB 481 SANNVVYKQYEDMVVESCGR 495

RESULT 4
B55452
cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999
C:Accession: B55452
R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Ko
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming gr
A:Reference number: A55452; MUID:95050604
A:Accession: B55452
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-436 <CHA>
A:Cross-references: GB:U13661; NID:g632489; PID:g632490

Query Match 33.9%; Score 905.5; DB 2; Length 436;
Best Local Similarity 42.5%; Pred. No. 1.2e-53;
Matches 206; Conservative 65; Mismatches 109; Indels 105; Gaps 16;

QY 67 GGATNANAKGGTGTGGLTQPKKDEPKKLPVPPGGPKPGHPPTQQTAR 126
DB 7 GSAKGMTRKEGRMPRA-----PRENATREPLDRQPPRPQEEPPQR----- 51
QY 127 QLPGGKAPKAGSVPSFLLKKAREPGPPPREPKPPPPPTPHEYMLSLYRTLSDADRK 186

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QY 281 RSYPLDGSWEVDIWKLFNRKNSAQLCLEAW-----ERGRAVDLRLGLGFDRAAR 334
Db 197 RLVHH-NESKWSFDVTP-----AIARWIAHQPNHGFEVFTHLND---K 239
QY 335 QVHEKALFLVFGTKRDLF--FNEIKARSGODDKTVYELFSQRKRRAPLATROGRKP 392
Db 240 NVPKHHVRSRSLTPKDNWPIRLVTFESHGK---GHALHKROKRA---RHQKR- 292
QY 393 SNLKKARSKALHVNFKDMGWDWIIAPLEYAFHCEGLCFPLRSHLEPTNHAVIQL 452
Db 292 -KRLKSCRRHPLVDFSDVGWMDWIVAPGYHAFYCHGCEPPLADHLNSTHNAIVQL 350
QY 453 MNSMDPESTPPTCCVPTLSPISILFDSANNVYKQYEDMVVESCGR 501
Db 351 VNSVN-TNIPKACCVPTLSAISMVLDENKVLKNYQDMVVEGCGR 398
RESULT 8
S45355
bone morphogenetic protein-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
C:Accession: S45355
R:Feng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Mundy, G.R.; Harris, S.E.
Biochim. Biophys. Acta 1218, 221-224, 1994
A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comp
A:Reference number: S45355; MUID:94289485
A:Accession: S45355
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <FEN>
C:Superfamily: inhibin
Query Match 16.6%; Score 443.5; DB 2; Length 394;
Best Local Similarity 32.8%; Pred. No. 8.8e-23;
Matches 131; Conservative 48; Mismatches 118; Indels 103; Gaps 19;
QY 142 SSFLKKAREGPPRPKPPFPPTTPHEYMLSLYRTLSADARKGNSSV-----KLE- 196
Db 58 SMFLKQR-----PTPSKDVVPP-----YMLDLYR-----RHSGQGPAPADHRLER 100
QY 196 -AGLANTITSF-----IDKQDGRGPVVKQRYVDFDISALEKDGLL-GAELRLKPKPSD 248
Db 101 AASRAMTVRTFHHEVAEPELPEMSGKTAR--RFFFLNLSVPDEFILTSAELOIFREQIOE 158
QY 249 T-----AKPAAGGGRAAQLKSSCPSGROPASLLDVRSPVGLDGSWEV 293
Db 159 ALGNSFSQHRINIYEIKPA-----AANKLF---PVTR---LLDTRLV-NQNTSOWES 204
QY 294 FDIWKLFNRKNSAQ-----LCLELEAWERGRAVDLRLGLGFDRAARQVHE-----KAL 341
Db 205 FDTVAVMRWTQGTNHNHGVVEVAHLEENPGVSKRHV---RISRLHQDEHSWSQIRPL 261
QY 342 FLVFGTKRDLFFNFIKARSGODDKTVYELFSQRKRRAPLATROGRKPKNLKARCS 401
Db 262 LVTFEGHDGK-----GHPLHKREKROAKHKQR-----KRLKSSCK 295
QY 402 RKALHVNFKDMGWDWIIAPLEYAFHCEGLCFPLRSHLEPTNHAVIOTLMNSMDPEST 461
Db 296 RHPLVDFSDVGWMDWIVAPGYHAFYCHGCEPPLADHLNSTHNAIVQLVNSVN-SKI 354
QY 462 PPTCCVPTLSPISILFDSANNVYKQYEDMVVESCGR 501
Db 355 PRACCVPTLSAISMVLDENKVLKNYQDMVVEGCGR 394
RESULT 9
BMH02
bone morphogenetic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 2A; rhBMP2
C:Species: Homo sapiens (man)

C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 05-Sep-1997
C:Accession: B37278; PC2178
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.;
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730
A:Accession: B37278
A:Molecule type: mRNA
A:Residues: 1-396 <WO2>
A:Cross-references: GB:M22489; NID:gl79501; PID:gl79502
R:Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Kat
J. Biochem. 115, 279-285, 1994
A:Title: Expression and characterization of human bone morphogenetic protein-2 in sil
A:Reference number: PC2178
A:Accession: PC2178
A:Molecule type: protein
A:Residues: 290-295, 'X', 297-304 <ISH>
A:Experimental source: cell line BoMo-15ALIC
R:Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J.
Protein Sci. 4 (Suppl.2), 443S, 1995
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (BMP-2
A:Reference number: A56729
A:Contents: annotation
A:Note: determination of amino ends of mature forms; dimers with long form chains hav
C:Comment: This hormone is capable of inducing bone formation at ectopic morphologica
C:Genetics:
A:Gene: GDB:BMP2; BMP2A
A:Cross-references: GDB:125204; OMIM:112261
A:Map position: 20p12-20p12
C:Complex: homodimer, disulfide linked
C:Superfamily: inhibin
C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-265/Domain: propeptide #status predicted <PRO>
F:266-396/Product: bone morphogenetic protein 2, long form #status predicted <MATL>
F:283-396/Product: bone morphogenetic protein 2 #status predicted <MAT>
F:135,163,164,200/Binding site: carboxylate (Asn) (covalent) #status predicted
F:283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
F:338/Binding site: carboxylate (Asn) (covalent) #status experimental
Query Match 16.5%; Score 440.5; DB 1; Length 396;
Best Local Similarity 30.6%; Pred. No. 1.4e-22;
Matches 136; Conservative 61; Mismatches 149; Indels 99; Gaps 19;
QY 94 PKLPPRPGPEPRKPPQTPQTARTVTPEKGLPGGKAPPKAGSVPSFLKKAREPG 153
Db 14 POVLGGAGLVPELG---RRKFAAASSGRFSSQ-----PSDEVLSFEFLRLSMFG 62
QY 154 PPREKPEFRPPPTTPHEYMLSLYRTLS-DADRGKGNSSVKLEAGLANTITSF-----ID 207
Db 63 LKQRP-TPSRDAVVP--YMLDLYRRHSGQSPAPDHLRLERAASRANTVRSFHHEESLE 119
QY 208 KGQDRGPVVKQRYVDFISAL-EKDGLLGAELRLTKPKPSDT-----A 250
Db 120 ELPETSGLTTR--RFFFLNLSIPTFEETISAELOVFEQMDALGNSSSFHHRINIYII 177
QY 251 KPAAPGGRAAQLKSSCPSGROPASLLDVRSPVGLDGSWEVDFIWKLFNRKNSAQ-- 309
Db 178 KPATAN-----SKFPVTR---LLDTRLV-NONASRWESFDVTPAVNRW--TAQGH 221
QY 309 ---LCLELEAWERGRAVDLRLGLGFDRAARQVHE-----KALFLVFGTKRKRDLFFN 356
Db 222 ANHGFVVEVAHLEEKQGVSKRHV---RISRLHQDEHSWSQIRPLLVTFEGHDGK----- 273
QY 357 EIKARSGODDKTVYELFSQRKRRAPLATROGRKPKNLKARCSKALHVNFKDMGWD 416
Db 273 -----GHPLHKREKROAKHKQR-----KRLKSSCKRHPLVYDFSDVGWMD 312
QY 417 WIIAPLEYAFHCEGLCFPLRSHLEPTNHAVIOTLMNSMDPESTPPTCCVPTLSPISI 476
Db 313 WIVAPPGYHAFYCHGCEPPLADHLNSTHNAIVQLVNSVN-SKIPKACCVPTLSAISM 371

QY 477 LFIDSANNVYKQYEDMVVESCGR 501
 Db 372 LYLDENEKVLKYNQDMVVECCGR 396

RESULT 10

bone morphogenetic protein 2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
 C:Accession: S37073
 R:Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
 submitted to the EMBL Data Library, September 1993
 A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein
 A:Reference number: S37073
 A:Accession: S37073
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-393 <FEN>
 A:Cross-references: EMBL:Z25868; NID:g397950; PID:g397951
 C:Superfamily: inhibin

Query Match 16.5%; Score 440.5; DB 2; Length 393;
 Best Local Similarity 31.7%; Pred. No. 1.4e-22;
 Matches 133; Conservative 54; Mismatches 131; Indels 101; Gaps 19;

QY 137 AGVSPSFLKAKREPGRPREKPF-----RPP-----TPHEYMUSLY 177
 Db 22 AGLPELGRKKFAGASRPSSEDLSEFELRLLSMFLGLKRLTPSKDVVPVPPMLDLY 81
 QY 178 RTLSADARKGNSSV-----KLE--AGLANTITSF-----IDKQDGRGVRKQRYVFD 225
 Db 82 R-----RHSGQPGALAPDRLEAASRANTVLSFHHEAIEELSEMSTSR--REFFN 133
 QY 226 ISALEKDGLL--GAELIRILKPKSDTAKPAAPGGGAAQLKLS-----SCPSGRQPAS- 277
 Db 134 LSSVPTDEFLTSAELQIFRQMEAL-----GNSFQHRINIYELIKPATASKFPVTR 187
 QY 277 LLDVRSVPGDGGSGWEVFDIWKLFNRKNSAQ-----LCELEAWERGRAVDLRGLGFD 330
 Db 188 LLDRLVT-QNTSOWESFDVTPAVMRW--TAQHTNHGFVVEVAHLEKPKGVSKRHV--- 242
 QY 331 RAARQVHE-----KALFLVFGRTKKRLDFFNEIKARSGODDKTYVEYLFSSORRERA 382
 Db 242 RISRLHODEHSWQVRPLVITFGHDK-----GHLHKREKROA 281
 QY 383 PLATROGRKPSKNLKARCSRKALHVNFKDMGWDWIITAPLEYAFHCEGLCEPPLRSHLE 442
 Db 282 KHKQR-----KRLKSSCKRHPLVDFSDVGNWDWIIVAPGYHAFYCHGCPPLADHLN 335
 QY 443 PTNHAIVQTLNMSMDPESTPTCCVPRRLSPISILFIDSANNVYKQYEDMVVESCGR 501
 Db 336 STNHAIVQTLNVSNN-SKIPKACCCVPTLSAISMLYLDENEKVVYKYNQDMVVECCGR 393

RESULT 11

BMH06
 bone morphogenetic protein 6 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Sep-1998
 C:Accession: B39263
 R:Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, J.; Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
 A:Title: Identification of transforming growth factor beta family members present in bone morphogenetic protein 6 precursor
 A:Reference number: A39263; MUID:91088608
 A:Accession: B39263
 A:Molecule type: mRNA
 A:Residues: 1-513 <CEL>
 A:Cross-references: GB:M60315; GB:M38694; NID:g339561; PID:g339562
 C:Genetics:
 A:Gene: GDB:BMP6
 A:Cross-references: GDB:127596; OMIM:112266

A:Map position: 6pter-6qter
 C:Superfamily: inhibin
 C:Keywords: bone; glycoprotein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-374/Domain: propeptide #status predicted <PRO>
 F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
 F:241,269,386,404,454/Binding site: carbohydrate (Asn) #status predicted

Query Match 16.2%; Score 434; DB 1; Length 513;
 Best Local Similarity 27.4%; Pred. No. 5.1e-22;
 Matches 156; Conservative 69; Mismatches 197; Indels 148; Gaps 25;

QY 12 WYLAWLDELFICTVLCAPDLGQRPQTRPGLAKAEKERPPPL-ARNVFRPGHSYGGGAT 70
 Db 10 WLCWMMGL--LCSCCGPPL-----RPLPAAAAAAGGOLLGDS 49
 QY 71 NANARAKGGTGTGG-----LTQPKDBPKKLPPRGGP-EPKPGH-----PPOTRQ 116
 Db 50 PGTEQPPSPQSSSGFLYRLUKTQEKREMKELISVLGPHRPLHGLQOPPPALRQ 109
 QY 117 ATARTVTPKQPLPGKAPKAGVPSS--FLL-----KKAKEPPGPPRE- 158
 Db 110 QEEQ--OQQQLPRGEP--GRKXAPLFLMLDLYNALSADNEDCAGSEGRQOSWPHEA 165
 QY 158 --PKFPRPPPTPHEYMLSLYRTLSADARKGNS--SVKLEAGL--ANTITSFIDKGO 210
 Db 166 ASSORRQPPPGAHP--LNRKSLAPGSGGASPLTSAQDSAFNDADVMVSYNLVE 223
 QY 211 DDR--GPVYRKOR-VYFDISAL--EKDGLLGAELIRILKPKSDTAKPAAPGGGAAQLKLS 266
 Db 224 YKESFPRORHHKEFNLSQIEGEGVWTAEEFRIY-----KDCVMGSKNQTFILIS 275
 QY 267 SCPSGRQ-----PASLLDVRSVPGDGGSGWEVFDI-----WKLFRFNKNSAQLCLELE 314
 Db 276 IYQVLQEHQHRDSDLFLDTRVWVASE--EGWLEFDITATSNLWVTPQHNMGLQLSV--- 332
 QY 315 AWEGRGAVDLRGLGDFRARAQVHEKALFLVFGRTKKRDLLFNEIKARSGODDKTYVEYLF 374
 Db 332 -----VTRDGVHVHPRAAGLV-----GRDGPYDKQPFMVAE 362
 QY 375 SQ-----RKRRAPLATRQGR-----PSKNLKARCSRKALHVNFK 410
 Db 363 FKVSEVHVITTSASSRRQQRNRSTQSDVARVSSASDYNSELKTACRKHELIVSFQ 422
 QY 411 DMGWDWIITAPLEYAFHCEGLCEPPLRSHLEPTNHAIVQTLNMSMDPESTPTCCVPR 470
 Db 423 DLGQDWIITAPKYAANYCDGECSPFLNAHMNATNHAIVQTLVHLMNPEVVPKPCCAPTK 482
 QY 471 LSPISILFIDSANNVYKQYEDMVVESCGR 500
 Db 483 LNAISVLYFDDNSNVILKKRYNNMVRACGC 512

RESULT 12

150608
 bone morphogenetic protein 4 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Feb-1997
 R:Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.
 Development 120, 209-218, 1994
 A:Title: Bone morphogenetic proteins and a signalling pathway that controls pattern in the chick embryo
 A:Reference number: 150607; MUID:94163974
 A:Accession: 150608
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-405 <FRA>
 A:Cross-references: EMBL:X75915; NID:g472929; PID:g472930
 C:Genetics:
 A:Gene: Bmp-4
 C:Superfamily: inhibin

Query Match 16.2%; Score 433; DB 2; Length 405;
Best Local Similarity 30.4%; Pred. No. 4.6e-22;
Matches 123; Conservative 64; Mismatches 153; Indels 64; Gaps 14;
QY 125 KOQLPGKAPKAGVPSFSF-----LLKAREPGPPREPKEPPFPPTTITHEYMLSLYR 178
DB 39 QOAGSGRRSAQSHLLRGFETTLQMFGLRRPQPSKSAVIP-----SYMLDIYR 89
QY 179 TLSDADRGKGNSSVKLE-----AGLANITTSFIDKGDDRGD---VVRKQYVFDISALE 230
DB 90 LOSGEEERSLOEISLOXPERSASRANTVRSFHEHLESVPGPSEAPRIAFVFNLSVP 149
QY 231 KDGLLGA-ELRLRKPSDTAKPAAPGGRAAQLKSCPSGRQPA--SLLDVRSVPGLD 287
DB 150 DNEVSSBELRLYRQVEEPSAAMWGRFHRIYEVKMPKLSERSQAITRLDTRLVHH-N 208
QY 288 GSGWVFIDIKLFRNFKNSAQ-----LCLEAWERGRAVDLRLGLGFDRAARQVHE----- 339
DB 209 VTRWETEDVSPAVIRWTKDQPNHGLVIEVTHLQAQTHQGHVIRISLSLPGHGGDWAQ 268
QY 339 -KALFLVGRKTRKDLFTNEIKARSGDDKTVYELFSQRRKRRAPLATROGKPSKNLK 397
DB 269 LRPLLVTEGHDGRHAL-----TRARRSP--KHHGSR--KN-K 302
QY 398 ARCSKALHVNFKMGDDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIOTILMNSMD 457
DB 303 KNCRRHALYVDSVDGNDWIAPPGYAFYCHGDCPPLADHLNSTHAIIVOTILVNSVN 362
QY 458 PESTPPTCCVPTLSPISLTFIDSANNVYKQYEDMWVSCGCR 501
DB 363 -SSIPKACVPTLSAISMLYLDKVKVLYKNQYQWVVEGCGCR 405

RESULT 13
JH0688
bone morphogenetic protein 2II precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997
C:Accession: JH0688
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A:Reference number: JH0687; MUID:92378616
A:Accession: JH0688
A:Molecule type: mRNA
A:Residues: 1-398 <NTS>
A:Cross-references: GB:X63425; NID:g64583; PID:g64584
A:Experimental source: oocyte
C:Superfamily: inhibin
K:Keywords: glycoprotein
F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
F:137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 432; DB 2; Length 398;
Best Local Similarity 32.1%; Pred. No. 5.3e-22;
Matches 127; Conservative 62; Mismatches 143; Indels 64; Gaps 18;
QY 133 APPKAGVPSFLLKAREPGPPREP---KEPFRPPPTITHEYMLSLYRLSD--ADRGK 187
DB 40 SPQSQQVLDQFELLLNMFGLKRPTGKNVIPP-----YMLDLYHLHSAQLADDOG 93
QY 188 GNS---SVKLEAGLANITTSFIDKGDDRGVVRK---QRYVFDISALEKGLL-GAELR 240
DB 94 SSEVDYHMERASRANTVRSFHEHSEMEIEPESGKTIQREFFNLSIPDEBELVTSSEL 153
QY 241 ILRKPSDTAKPAAPGGRAAQLK-----SSCPGSRGP-ASLLDVRVPGLDGSGVEVF 294
DB 154 IFREQ---VQEPFKYDGSGLKRLHINIYDVKPAAASRGVVRLLDTRLIHH-NEKSWESF 209
QY 295 DIWKLFNRNFKNSAQLCLEAW-----ERGRAVDLRLGLGFDRAARQVH---EKALFLVF 345

Db 210 DVTP-----AITRWIAHKQPNHGFVVEVTHLNDNTNPKRHVIRISRLTLDK 256
QY 346 GRTKKRDLFFNEIKARSGDDKTVYELFSQRRKRRAPLATROGKPSKNLKARCSKAL 405
Db 257 GHWPFR---IRPLLVTFSDHGK---GHALKHQRKQA---RHQR---KRLKSSCRRHPL 303
QY 406 HVNFKMGDDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIOTILMNSMDPESTPTTC 465
Db 304 KYVDSVDGNDWIAPPGYHAFYCHGDCPPLADHLNSTHAIIVOTILVNSYN-TNPKAC 362
QY 466 CVPTLSPISLTFIDSANNVYKQYEDMWVSCGCR 501
Db 363 CVPTLSAISMLYLDKVKVLYKNQYQWVVEGCGCR 398
RESULT 14
S52408
SPDVRL protein - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
C:Accession: S52408
R:Ponce, M.R.; Micol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A:Description: SPDVRL, a member of the transforming growth factor-beta superfamily ex
A:Reference number: S52408
A:Accession: S52408
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <PON>
A:Cross-references: EMBL:Z48313; NID:g673496; PID:g673497

Query Match 16.0%; Score 428.5; DB 2; Length 461;
Best Local Similarity 29.7%; Pred. No. 1.1e-21;
Matches 129; Conservative 48; Mismatches 105; Indels 153; Gaps 17;
QY 163 RPPPTITHEYML-----SLYRFLSDADRGKGNSSVKLEAG----- 198
DB 82 RPPSLRGQNOFCAOFTWYSYRTLNIDEQSGHPSETEPOPGGLASNAIYNPSDSSIGS 141
QY 198 -----LANTIITS---FIDKGDDRGVVRKQRYVFDISAL-EKDGL 234
DB 142 VMSGTFVNYTRNEVQVQADTMSLPVHYKDAIED-----TEHYRFDIGRIPQGETV 196
QY 235 LGAEILRLRKPSDTAKPAAPGGRAAQLKSCPSGRQPAFL--LDVRSY--PGLDGS- 290
DB 197 TSAELRVF-----DAGRQGRSLYRIDVLLRLRERSGDSR 231
QY 290 -----GWEVEDI-----WKLFRNFKNSAQLCLEAWERGRAVDLRLGLG 328
DB 232 SPVYLDSTIVGADHGLVDFDMSATSTWRSYPGANYGLQ-----RVESLQGLN 281
QY 329 FDRAARQVHEKALFLVFRGTRKKRD---LFFNEIKARSGDDKTVYELFSQRRKRAPL 384
DB 282 IDPTDAGV-----VGYNNEGREPFMVVF-----QRNEEVATINSHLRNRA-- 326
QY 385 ATRO---GKRPSK-----NLKARCSKALHVNFKMGDDWIIAPLEYE 425
DB 326 ATROKGGKRRPKPDTNDIASRDSASSLSNDWQCKRKNLFVNFEDLDWQEWIAPLYV 385
QY 426 AFHCEGLCEPPLSHLEPTNHAVIOTILMNSMDPESTPTCCVPTLSPISLTFIDSANNV 485
DB 386 AFYCGGCAFLPHGANATNHAIIVOTLVHMSHSPVQPCCAPTKLSPTIYLYDSDSRV 445
QY 486 VYKQYEDMWVSCGCR 500
DB 446 VLKYYKNVVRACGC 460

RESULT 15
I49542
bone morphogenetic protein 5 - mouse
C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Feb-1997
C:Accession: I49542
R:King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.
Dev. Biol. 166, 112-122, 1994
A:Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice
A:Reference number: I49542; MUID:95046894
A:Accession: I49542
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-452 <RES>
A:Cross-references: GB:L41145; NID:g755033; PID:g755034
C:Genetics:
A:Gene: BMP5
C:Superfamily: inhibin

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Query Match      16.0%; Score 428; DB 2; Length 452;
Best Local Similarity 29.0%; Pred. No. 1.le-21;
Matches 140; Conservative 66; Mismatches 164; Indels 112; Gaps 20;

QY 76 AKGCTGQT-----GGLTOPKKDEPKK-----LP--PRGCGPEPKCHPP-----QT 114
Db 25 AKGLGDNHVSSTYRLNRHERREITSLTGLPHRPFSPGKQASSAPLFMLDL 84

QY 115 RQATARTVTPKGQLP----GKAPPKAGSVSPFLKKKAREPGPREPKEPRPPITPH 170
Db 85 YNAMASEDNPEYLVYRSLAGEAKETRGYPASNGYAHRLHLPRTLTQSP----- 140

QY 171 EYMLSLYRT--LSADRRKGNSSVKLEAGLANTITSIDKQDDRGVPVVRKQRYV---FD 225
Db 140 --LASLHDTNFDNAD-----MVMSEFNLVERDKDFSHQRRHYKEFRFD 181

QY 226 ISAL-EKDGLLGAELRLRKPSDTAKPAAPGGGAAQ--LKLSSCPSGROPAS----- 277
Db 182 LTQIPHGEAVTAAPFRIYKDK-----GNHRFENETIKISYQIKEYITNRDADLF 231

QY 277 LLDVRSVPGLDGGGWEVFDI-----WKLFRNFKNSAQLCLEAWERGRAVDLRGLG-- 329
Db 232 LLDTRKQALD-VGWLVDIIVTNSHHVINPONNLGLQLCAET---GDGRSINVKSAGLV 287

QY 329 -----FDRAARQVHEKALFLVFGRTKKRDLFTNEIKARSGQDDKTVYELFSQRR 378
Db 288 GRHGPOSKQPEWMAFFRASEVLLRSVRAASKKKNQ--NRNKSNSHQDPS----- 335

QY 379 KRAPLATRQGRPSKNLKAACRSKALHVNFKDMGDDWIIIAPLEYAFHCEGLCEPPLR 438
Db 335 --RMPSA---GDYNTSEOKQACKKHELYVSPRDLGWQDWIIIAPEGYAFYCDGECSPFLN 389

QY 439 SHLEPTNHAIVQTLNMSMDPESTPTCCVPTRLSPISLTFLDSANNVYKQYEDMVVESC 498
Db 390 AHMNATNHAIVOTLVHLFPDPVPRPCCAPTKLNAISLVLPFDDSSNVLTKRYNNVVRSC 449

QY 499 GC 500
Db 450 GC 451
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Job time: 2063 sec

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